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(54) Title: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING CONDITIONS, DISORDERS, OR DIS-  
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(57) Abstract:

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# PATENT COOPERATION TREATY

## PCT

### DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT (PCT Article 17(2)(a), Rules 13ter and 39)

Applicant's or agent's file reference 10001-006-228	<b>IMPORTANT DECLARATION</b>	Date of mailing (day/month/year) <b>17 JUL 2001</b>
International application No. PCT/US01/11655	International filing date (day/month/year) 09 APRIL 2001	(Earliest) Priority Date (day/month/year) 11 APRIL 2000
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.		
Applicant COGENT NEUROSCIENCE, INC.		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
  - a. ☐ scientific theories.
  - b. ☐ mathematical theories.
  - c. ☐ plant varieties.
  - d. ☐ animal varieties.
  - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
  - f. ☐ schemes, rules or methods of doing business.
  - g. ☐ schemes, rules or methods of performing purely mental acts.
  - h. ☐ schemes, rules or methods of playing games.
  - i. ☐ methods for treatment of the human body by surgery or therapy.
  - j. ☐ methods for treatment of the animal body by surgery or therapy.
  - k. ☐ diagnostic methods practiced on the human or animal body.
  - l. ☐ mere presentations of information.
  - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☒ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
 

☒ the description
☒ the claims
☒ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out.
 

☒ the written form has not been furnished or does not comply with the standard.

☐ the computer readable form has not been furnished or does not comply with the standard.
4. Further comments:  
Please See Continuation Sheet.

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Form PCT/ISA(2003) (July 2003) \*  
Washington, D.C. 20531

Authorized officer

MARY TUNG (703) 308-0196

DECLARATION OF NON-ESTABLISHMENT OF  
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435/7.1, 69.1, 91.1, 252.5, 320.1; 514/12, 44; 536/23.5

4. Further Comments (Continued):

A meaningful search cannot be performed on the instant claims.  
The claims appear to encompass an unfathomable number of inventions because of the number of claimed sequences.

It is noted that the instant claim set is apparently drawn to a multitude of DNA or amino acid sequences shown in Figures 4-13. Each of Figures 4-13 are apparently broken up into a multitude of subfigures. Claim 1 (a) apparently refers to "an amino acid sequence which is shown in all of Figures 4A-AB". It is not at all clear how one sequence can be the same as all those separate, distinct sequences. Perhaps applicant intended to refer to the various subfigures in the alternative? Or maybe the open claim language "comprising" as in an amino acid sequence which comprises all of those shown in Figures 4A-AB.

Figures 4-13 are defective because the sheets are not numbered in consecutive Arabic numbers. See PCT/RO/106 mailed May 4, 2001. Further, the first sheet of each of the Figures 4-13 contains a heading "open reading frame for..." and the text "Fig No." These words are missing from the subsequent sheets of each of the subfigures 4-13. The figures are not clearly labeled. Further, with regard to the headings, PCT Rule 11.11(a) prohibits words in the drawings.

Each figure does not have a unique label which says "Fig. No. 4A, Figure No. 4B", etc. Some of the figures apparently contain subfigures which run over onto the next sheet. See 10L, 10J, etc. Further, some of the figures apparently contain subfigures which do not have a figure label, see the text in the box above Figure 10P. Furthermore, the numbering system of the sequences appears to be incorrect, see numbers 340 and 341, both denoting the same position of the last line of amino acids of Figure 10H. None of the aberrations are permissible and a search of any such material would not be meaningful.

Beyond all these errors, the overriding problem with performing a search on the claims is that in the figures and of the Brief Description of the Figures, pages 13-15, no SEQ ID Nos are provided. Without any such correlation, it is impossible to determine which of the sequences recited in the claims correspond to those recited in the sequence listing. Absent that correlation, it is impossible to determine the full scope of the claimed invention or to search even a portion of the claimed invention.

PCT Rule 6.2(a) states that the claims shall not, except when absolutely necessary, rely, in respect to the technical features of the invention, on references to the description of the drawings. In particular, they shall not rely on such references as "as described in part...of the description" or "as illustrated in figure...of the drawings". The nature of the instant invention does not meet the criteria of "absolutely necessary" because these claims could have easily been drafted to include the particular SEQ ID Nos of the sequences. That may result in the claim becoming rather lengthy, but this is to be expected when one claim appears to encompass hundreds of inventions.

The Authorized Officer contacted the applicants on 16 May 2001 concerning a potential Lack of Unity. However, upon further consideration, the claims have been determined to be unsearchable.





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EASES INVOLVING CELL DEATH

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**COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING  
CONDITIONS, DISORDERS, OR DISEASES INVOLVING CELL DEATH**

**1 INTRODUCTION**

The present invention relates to compositions and methods for the treatment and diagnosis of conditions, disorders, or diseases involving cell death, including, but not limited to, neurological disorders such as stroke. Nucleic acids are described herein which, when introduced into a cell either predisposed to undergo cell death or in the process of undergoing cell death, prevent, delay, or rescue the cell from death relative to a corresponding cell into which no exogenous nucleic acids have been introduced. Such nucleic acids are referred to as "protective sequences". Protective sequences or their products are identified by their ability to prevent, delay, or rescue a cell, cells, tissues, organs, or organisms from dying. Protective sequences or their products are also identified via their ability to interact with other genes or gene products involved in conditions or disorders involving cell death.

The invention further includes recombinant DNA molecules and cloning vectors comprising protective sequences, and host cells and host organisms engineered to contain such DNA molecules and cloning vectors. The present invention further relates to protective sequence products and to antibodies directed against such protective sequence products.

The protective sequences identified, their products, or antibodies may be used diagnostically, prophylactically, therapeutically or as targets for therapeutic intervention. In this regard, the present invention provides methods for the identification and prophylactic or therapeutic use of compounds in the treatment and diagnosis of conditions, disorders, or diseases involving cell death. Additionally, methods are provided for the diagnostic monitoring of patients undergoing clinical evaluation for the treatment of conditions or disorders involving cell death, for monitoring the efficacy of compounds in clinical trials and for identifying subjects who may be predisposed to such conditions, disorders, or diseases involving cell death.

## 2 BACKGROUND OF THE INVENTION

### 2.1 Mechanisms which Lead to Cell Death

It is widely recognized that at least two distinct cell death mechanisms exist for mammalian cells. These two mechanisms are necrosis and apoptosis, and are significant components of numerous conditions, disorders and disease states.

Necrosis plays an important physiologic role in signaling the presence of certain conditions. When cells die as a result of necrosis, the dying cells release substances that activate the body's immune response in a local, and in some cases widespread, reaction to the necrosis-inducing condition. This response is important in, for example, bacterial infection.

Experimental evidence in a wide variety of cells throughout the body has revealed that every cell can initiate a program of self-destruction, called apoptosis. This program can be initiated by a wide variety of natural and unnatural events. There are at least four distinct pathways for executing this program of cell death, and it is virtually certain that dozens, if not hundreds, of different intracellular biochemical cascades interact with each pathway. It is equally likely that certain cell types, such as cells in the heart or neurons, will utilize specialized signaling pathways that are not generally represented elsewhere in the body. However, since cell death is neither always necessary nor desired, it would be desirable to manipulate the manner in which cells start their death process. In some circumstances, preventing, delaying, or rescuing cells from death would either alleviate the disease or allow more time for definitive treatment to be administered to the patient. An example of this situation is brain cell death caused by ischemic stroke: preventing, delaying, or rescuing cells from death until the blood supply to the brain could be restored would greatly reduce, if not eliminate, the possibility of a person's death and/or long-term disability from stroke (Lee JM, et al. *Nature* 1999, 399(supp): A7-A14; Tarkowski E, et al. *Stroke* 1999, 30(2): 321-7; Pulera MR, et al. *Stroke* 1998, 29(12): 2622-30). In still other circumstances, the failure of cells to die may itself lead to disease such as cancer (Hetts SW. *JAMA* 1998, 297(4): 300-7).

Cell death plays an important role in the normal function of mammalian organisms. While it may seem counterintuitive for cells to have death as a normal part of their life cycle, controlled and physiologically appropriate cell death is important in regulating both the absolute and relative numbers of cells of a specific type. (Hetts SW. *JAMA* 1998, 297(4):

300-7; Garcia I, et al. *Science* 1992, 258(5080): 302-4). When the mechanism of apoptosis does not function properly and normal cell death does not occur, the resulting disease is characterized by unregulated cellular proliferation, as occurs in a neoplastic disease or an autoimmune disease (Hetts SW. *JAMA* 1998, 297(4): 300-7; Yachida M, et al. *Clin Exp Immunol* 1999, 116(1): 140-5).

One method for regulating cell death involves manipulating the threshold at which the process of cell death begins. This threshold varies significantly by cell type, tissue type, the type of injury or insult suffered by the cell, cellular maturity, and the physiologic conditions in the cell's environment (Steller H., *Science* 1995, 267(5203): 1445-9). Although it is probable that certain cellular injuries or insults irrevocably induce death, lesser injuries or insults may begin the dying process without inducing irreversible cell death. What constitutes a lesser injury or insult may vary tremendously with changes in the factors influencing that cell's death threshold. The ability to alter a cell's threshold for responding to an injury or insult, that is, to either promote or discourage cell death, would be a desirable goal for the treatment of conditions involving cell death. The ability to better control cell death, by either discouraging or promoting the mechanisms of cell death, would be an important invention for ameliorating disease (US Patents 5,925,640; 5,786,173; 5,858,715; 5,856,171).

Recent evidence suggests that the mechanisms of cellular death may be more complex than the two discrete pathways of apoptosis and necrosis. Examples of this evidence may be found in the central nervous system (CNS). In the complex CNS cellular environment, both necrosis and apoptosis are observed with commonly studied conditions, disorders, or diseases such as focal ischemia, global ischemia, toxic insults, prolonged seizures, excitotoxicity, and traumatic brain injury. In some reports, both apoptosis and necrosis have been described (Choi WS, et al. *J Neurosci Res* 1999, 57(1): 86-94; Li Y, et al. *J Neurol Sci* 1998, 156(2): 119-32; Lee J-M, et al. *Nature* 1999, 399(supp): A8-A14; Baumgartner WA, et al. *Ann Thorac Surg* 1999, 67(6): 1871-3; Fujikawa DG, et al. *Eur J Neurosci* 1999, 11(5): 1605-14; Gwag BJ, et al. *Neuroscience* 1999, 90(4): 1339-48; Mitchell IJ, et al. 1998, 84(2): 489-501; Nakashima K, et al. *J Neurotrauma* 1999, 16(2): 143-51; Ginsburg, MD *Cerebrovascular Disease: Pathophysiology, Diagnosis, and Management* 1998 Ch 42; Rink AD, et al. *Soc Neurosci Abstr* 1994, 20:250(Abstract)). Similar observations also occurred with brain tumor cells. (Maurer BJ, et al. *J Natl Cancer Inst* 1999, 91(13): 1138-46)

Other investigators found that neurons die by either apoptosis or necrosis under different environmental conditions (Taylor DL, et al. *Brain Pathol* 1999, 9(1): 93-117). There also are reports of a unique type of neuronal cell death following stroke. This new type of cell death has features common to both necrosis and apoptosis (Fukuda T, et al. *Neurosci Res* 1999, 33(1): 49-55). Other investigators believe that neuronal cell death is best represented by a continuum between apoptosis and necrosis, possibly mediated by calcium levels (Lee J-M, et al. 1999, 399(supp): A7-A14), or a combination of direct ischemic damage followed by indirect damage from excitotoxicity and loss of interneuronal connections (Martin LJ, et al. *Brian Res Bull* 1998, 46(4): 281-309). Further complicating the picture of neuronal cell death is the observation that the death of one or more neurons in one region of the brain can induce the death of neurons in other brain regions. This phenomenon has been observed with stroke as described above (Martin LJ, et al. *Brain Res Bull* 1998, 46(4): 281-309) as well as neuronal cell death induced by the withdrawal of growth factors (Ryu BR, et al. *J Neurobiol* 1999, 39(4): 536-46). Given the complex nature of actions and interactions among the many physiologic and molecular forces in brain tissue, and the different abilities of many substances acting either alone or in combination to induce cellular injury or death, it is difficult to determine with any degree of certainty if a nerve cell death process is due to apoptosis or necrosis (Graham DI, *Greenfield's Neuropathology* Ch 3 1997).

Despite the challenges in classifying the mechanism of cellular death, there is broad agreement that most, if not all, cells share common features in their death mechanisms (see, e.g., Lee J.M., et al., *Nature* 1999, 399 (supp): A7-A14).

## 2.2 Selected Factors and Conditions which Inhibit Cell Death Mechanisms

Several factors have been reported to inhibit the cell death pathway. One of the best-known factors is the gene product *bcl-2* (Adams JM, et al. *Science* 1998, 281(5381): 1322-6; Vaux DL, et al. *Proc Natl Acad Sci* 1993, 90(3): 786-9; US Patent 5,856,171 and references cited therein). Expression of *bcl-2* is believed to regulate apoptotic death in neurons, kidney, heart, liver, blood and skin cells under experimental conditions. In addition to regulating death by apoptosis, *bcl-2* is believed to regulate death caused by non-apoptotic mechanisms. Factors related to *bcl-2* have been shown to be over-expressed in cancer and autoimmune conditions, disorders, or diseases (US Patent 5,856,171 and references cited

therein). Other related factors acting on the same pathway as *bcl-2* also delay or prevent cell death.

In the brain, several factors have been shown to influence the cell death pathway. In excitotoxic injury to neurons, it was shown that lithium or *bcl-2* each individually protected neurons against cell death (Nonaka S, et al. *Proc Natl Acad Sci* 1998, 95(5): 2642-7; Behl C, et al. *Biochem Biophys Res Commun* 1993, 197(2): 949-56). During ischemic injury to neurons, it was shown that nerve growth factor (NGF) and *bcl-2* individually offered protection against neuronal death (Guegan C, et al. *Neurobiol Dis* 1999, 6(3): 180-9; Linnik MD, et al. *Stroke* 1995, 26(9): 1670-4).

Factors acting to prevent cell death do not act solely in the brain. In the heart, increased tolerance to non-lethal ischemic injury was associated with an increased expression of the *bcl-2* gene, suggesting that *bcl-2* was involved in protecting the cardiac muscle cells against ischemic injury (Maulik N, et al. *Ann NY Acad Sci* 1999, 874:401-11). This same study demonstrated that lower levels of *bcl-2* expression were associated with higher rates of cardiac cell death. A similar result was found for mechanical injury to heart papillary muscle cells.

Recently, it has been demonstrated that *bcl-2* prevented cell death in a brain ischemia model (Guegan C, et al. *Neurobiol Dis* 1999, 6(3): 180-9; Linnik MD, et al. *Stroke* 1995, 26(9): 1670-4). It was shown that the activity of *bcl-2* to prevent neuronal death was consistently demonstrated across several different physiologic insults. It also has been demonstrated that the distinction between apoptotic death and necrotic death is open to question, so the possibility exists that *bcl-2* can prevent or delay the necrotic cell death pathway, the apoptotic cell death pathway or perhaps an as yet undemonstrated cell death pathway.

Preventing cell death is an important medical goal. Several types of mammalian cells, most notably neurons and cardiac muscle cells, have limited if any capacity to regenerate. Preventing the death of these cells from conditions such as heart attack, stroke, shock, infection, cancer, Alzheimer's disease or traumatic injury, to name a few, would be an important medical advance as the heart and brain cannot grow sufficient cells to replace those cells lost to disease or infection.

In addition to preventing cell death, delaying and/or rescuing cells from programmed cell death is also an important medical goal. In many pathological conditions where there is an expectation that the disease will be successfully treated, such as many types of infection, hypoxia, ischemia or metabolic disturbances, delaying cell death would allow the pathological condition to be treated without permanent damage to the cells. In other words, the cells may be put into a suspended state from which they could successfully be rescued and emerge with their normal function intact.

### 3 SUMMARY OF THE INVENTION

The present invention relates to the discovery, identification and characterization of protective sequences and to compositions and methods for the treatment and diagnosis of conditions, disorders, or diseases involving cell death. Protective sequences refer to nucleic acid molecules comprising nucleic acid sequences which, when introduced into a cell either predisposed to undergo cell death or in the process of undergoing cell death, prevent, delay, or rescue the cell from death relative to a corresponding cell into which no exogenous nucleic acids have been introduced. For example, protective sequences may act to prevent, delay, ameliorate, inhibit, reduce, or rescue neuronal cell death (*e.g.* apoptosis, necrosis and related cellular events). The invention further relates to the discovery, identification and characterization of gene products encoded by such nucleic acid molecules, or by degenerate, *e.g.*, allelic or homologous, variants thereof. Protective sequences also can be regulatory nucleic acids. Protective sequences further can be both coding sequences and regulatory sequences.

The invention further relates to target sequences. Target sequences include, but are not limited to, upstream and downstream regulatory sequences, upstream and downstream complete or partial gene or gene product sequences, antibodies, antisense molecules or sequences, ribozyme molecules, and other inhibitors or modulators directed against such protective sequences and protective sequence products.

Protective sequences and protective sequence products can be utilized prophylactically and/or therapeutically to prevent, delay ameliorate, inhibit, reduce, or rescue conditions of cell death or symptoms of conditions, disorders, or diseases involving cell death. The modulation of the expression of protective sequences, *e.g.*, endogenous protective

sequences, and/or the activity of the protective sequence products, *e.g.*, endogenous protective sequence products, can also be utilized prophylactically or therapeutically to prevent, delay, ameliorate, inhibit, reduce, or rescue conditions of cell death or symptoms of conditions, disorders, or diseases involving cell death. Further, protective sequences and protective  
5 sequence products can be used to diagnose individuals exhibiting or predisposed to such conditions, disorders, or diseases involving cell death.

The compositions of the present invention include, in particular, nucleic acid molecules which comprise the following sequences: (a) nucleic acids of protective sequences, as well as allelic variants, homologs, mutants and fragments thereof; (b) nucleic acids which  
10 encode protective sequence products; (c) nucleic acids which encode protective sequence regulatory elements; (d) nucleic acids which encode fusion proteins comprising protective sequence products or one or more protective sequence product domains fused to a heterologous polypeptide; (e) nucleic acids which encode fusion proteins comprising protective sequence regulatory elements fused to a heterologous polypeptide; (f) nucleic acids  
15 which hybridize to the above described sequences under highly stringent or moderately stringent conditions, including, but not limited to, human homologs; and (g) complementary (*e.g.*, antisense) nucleic acids of the sequences described in (a) through (f), above. The nucleic acid molecules of the invention include, but are not limited to, cDNA, genomic DNA (including non-expressed features such as introns) and RNA sequences.

The present invention also encompasses expression gene products of the protective sequences listed above; *i.e.*, proteins and/or polypeptides that are encoded by the above protective sequences. The present invention also encompasses expression gene products generated by differentially or alternately splicing the protective sequences listed above. Nucleic acid molecules that can separately encode these differentially or alternatively spliced  
25 gene products are also included in the invention.

Mimics, agonists and antagonists of the protective sequences, protective sequence products, genes, gene products, or their regulatory elements are also included in the present invention. Such mimics, agonists and antagonists will include, for example, small molecules, large molecules (*e.g.*, protective sequence product fragments or protective  
30 sequence product ligands) and antibodies directed against a protective sequence product. Mimics, agonists and antagonists of the invention also include nucleic acids, such as antisense



and ribozyme molecules, and gene or regulatory sequence replacement constructs, which can be used to modulate, inhibit or enhance expression of a protective sequence.

The present invention further encompasses cloning and expression vectors, which may include, but are not limited to, bacterial, fungal, insect, plant, and mammalian vectors, which contain the protective nucleic acid sequences of the invention, which can be used as probes or to express those protective nucleic acid sequences, protective sequence products, genes and/or gene products in host cells or organisms. The present invention also relates to cells that have been transformed, transfected, or infected with such vectors, and to cells engineered to contain or express the protective nucleic acid sequences, protective sequence products, genes, gene products, and/or regulatory elements of the invention. Further, non-human host organisms which have been transformed, transfected, or infected with these protective nucleic acid sequences, or their regulatory elements, are also encompassed in the present invention. Host organisms of the invention include organisms transformed, transfected, or infected with the cloning vectors described above, including, but not limited to, non-human transgenic animals, and particularly transgenic non-human mammals which have been engineered to express a protective sequence, protective sequence product, gene, gene product, or regulatory element of the invention, or "knock-outs" which have been engineered to not express the protective sequence, protective sequence product, gene, gene product, or regulatory element of the invention.

The transgenic animals of the invention include animals which express a mutant variant or polymorphism of a protective sequence, protective sequence product, gene, gene product, or regulatory element, particularly a mutant variant or polymorphism of a protective sequence, protective sequence product, gene, gene product, or regulatory element which is associated with a condition, disorder, or disease involving cell death. The transgenic animals of the invention further include those that express a protective sequence transgene at higher or lower levels than normal. The transgenic animals of the invention further include those which express the protective sequence, protective sequence product, gene, gene product, or regulatory element in all their cells, "mosaic" animals which express the protective sequence, protective sequence product, gene, gene product, or regulatory element in only some of their cells, and those in which the protective sequence, protective sequence product, gene, gene product, or regulatory element is selectively introduced into and expressed in a specific

cell type(s). The transgenic animals of the invention also include "knock-out" animals. Knock-out animals comprise animals that have been engineered to no longer express the protective sequence, protective sequence product, gene, gene product, or regulatory element.

The present invention also relates to methods and compositions for the  
5 diagnosis of conditions, disorders, or diseases involving cell death, as well as for the identification of subjects susceptible to such conditions, disorders, or diseases. Such methods comprise, for example, measuring expression of the protective sequence, protective sequence product, gene, gene product, or regulatory element in a patient sample, or detecting a mutation  
10 in the protective sequence, protective sequence product, gene, gene product, or regulatory element in the genome of a mammal, including a human, suspected of exhibiting such a condition, disorder, or disease. The protective nucleic acid molecules of the invention can be used also as diagnostic hybridization probes, or as primers for diagnostic PCR analysis to identify protective sequences, protective sequence products, genes, gene products, or  
15 regulatory element mutations, allelic variations or regulatory defects, such as defects in the expression of the protective sequence, protective sequence product, gene, gene product, or regulatory element. Such diagnostic PCR analyses can be used to diagnose individuals with a condition, disorder, or disease involving cell death associated with a particular protective sequence, protective sequence product, gene, gene product, or regulatory element mutation, allelic variation or regulatory defect. Such diagnostic PCR analyses can be used also to  
20 identify individuals susceptible to such conditions, disorders, or diseases involving cell death.

Methods and compositions, including pharmaceutical compositions, for the treatment of conditions, disorders, or diseases involving cell death also are included in the invention. Such methods and compositions can increase, decrease or otherwise modulate the level of protective sequences, protective sequence products, genes, gene products, or their  
25 regulatory elements in a patient in need of such treatment. Such methods and compositions can also modulate the level of protective sequence expression (*e.g.*, endogenous protective sequence expression) and/or the level of activity of a protective sequence product, (*e.g.*, endogenous protective sequence product). Further, since the protective sequence or protective sequence product need not normally be involved in such conditions, disorders, or diseases,  
30 such methods include, for example, modulating the expression of the protective sequence and/or the activity of the protective sequence product for the treatment of conditions,

disorders, or diseases involving cell death which are normally mediated by some other gene.

In one embodiment, such methods and compositions are utilized for the treatment of the types of conditions, disorders, or diseases, which can be prevented, delayed or rescued from cell death and include, but are not limited to, those associated with the central nervous system including neurological and psychiatric conditions, disorders, or diseases; those of the peripheral nervous system; conditions, disorders, or diseases caused by physical injury; conditions, disorders, or diseases of the blood vessels or heart; conditions, disorders, or diseases of the respiratory system; neoplastic conditions, disorders, or diseases; conditions, disorders, or diseases of blood cells; conditions, disorders, or diseases of the gastrointestinal tract; conditions, disorders, or diseases of the liver; conditions, disorders, or diseases of the pancreas; conditions, disorders, or diseases of the kidney; conditions, disorders, or diseases of the ureters, urethra or bladder; conditions, disorders, or diseases of the male genital system; conditions, disorders, or diseases of the female genital tract; conditions, disorders, or diseases of the breast; conditions, disorders, or diseases of the endocrine system; conditions, disorders, or diseases of the thymus or pineal gland; conditions, disorders, or diseases of the skin or mucosa; conditions, disorders, or diseases of the musculoskeletal system; conditions, disorders, or diseases causing a fluid or hemodynamic derangement; inherited conditions, disorders, or diseases; conditions, disorders, or diseases of the immune system or spleen; conditions, disorders, or diseases caused by a nutritional disease; and conditions, disorders, or diseases typically occurring in infancy or childhood, as described in Section 5.4.1.1. below.

In yet another embodiment, the methods and compositions of the invention are utilized for the prevention, or delay, of cell death in the event of one or more infections which may be caused by bacteria; viruses; members of the family rickettsiae or chlamydia; fungi, yeast, hyphae or pseudohyphae; prions; protozoans; or metazoans.

In a further embodiment, the compounds and methods of the invention can be used to treat infections or conditions, disorders, or diseases which cause cell death in organ systems including, but not limited to, blood vessels, heart, red blood cells, white blood cells, lymph nodes, spleen, respiratory system, oral cavity, gastrointestinal tract, liver and biliary tract, pancreas, kidney, lower urinary tract, upper urinary tract and bladder, male sexual organs and genitalia, female sexual organs and genitalia, breast, thyroid gland, adrenal gland, parathyroid gland, skin, musculoskeletal system, bone marrow or bones.

In another embodiment, the compounds and methods of the invention can be used to treat further physiological impacts on organs caused by the infections which induce cell death including, but not limited to, fever equal to or greater than 101.5 degrees Fahrenheit, a decrease or increase in pulse rate by more than 20 beats per minute, a decrease  
5 or increase in supine systolic blood pressure by more than 30 millimeters of mercury, an increase or decrease in respiratory rate by more than 8 breaths per minute, an increase or decrease in blood pH by more than 0.10 pH units, an increase or decrease in one or more serum electrolytes outside of the clinical laboratory's usual reference range, an increase or decrease in the partial pressure of arterial oxygen or carbon dioxide outside of the clinical  
10 laboratory's usual reference range, an increase or decrease in white or red blood cells outside of the laboratory's usual reference range, an acute confusional state such as delirium where delirium is defined by the American Psychiatric Association's DSM-IV Manual or a diminished level of consciousness or attention.

In another embodiment, the compounds and methods of the invention can be  
15 used to promote cell death. These compounds could be useful for treating and/or ameliorating conditions caused by, for example, cancer and autoimmune diseases, both of which are manifested by an uncontrolled growth of cells.

The invention still further relates to methods for identifying compounds which modulate the expression of a protective sequence and/or the synthesis or activity of a  
20 protective sequence product. Such compounds include therapeutic compounds which can be used as pharmaceutical compositions to reduce or eliminate the symptoms of conditions, disorders, or diseases involving cell death. Cellular and non-cellular assays are described which can be used to identify compounds which interact with a protective sequence, protective sequence product, gene, gene product, and/or regulatory element, *e.g.*, modulate the  
25 activity of a protective sequence and/or bind to a protective sequence product. Such cell-based assays of the invention utilize cells, cell lines, or engineered cells or cell lines that express the protective sequence, protective sequence product, gene, gene product, and/or regulatory element.

In one embodiment, such methods comprise contacting a compound to a cell  
30 which expresses a protective sequence, protective sequence product, gene, gene product, and/or regulatory element, measuring the level of protective sequence expression, gene

product expression or gene product activity, and comparing this level to the level of protective sequence expression, gene product expression or gene product activity produced by the cell in the absence of the compound, such that if the level obtained in the presence of the compound differs from that obtained in its absence, a compound which modulates the expression of the protective sequence and/or the synthesis or activity of protective sequence products has been identified.

In an alternative embodiment, such methods comprise administering a compound to a host, *e.g.*, a transgenic animal which expresses a protective sequence transgene or a mutant protective sequence transgene, and measuring the level of protective sequence expression, gene product expression or gene product activity. The measured level is compared to the level of protective sequence expression, gene product expression or gene product activity in a host which is not exposed to the compound, such that if the level obtained when the host is exposed to the compound differs from that obtained when the host is not exposed to the compound, a compound which modulates the expression of the protective sequence and/or the synthesis or activity of protective sequence products, and/or the symptoms of conditions, disorders, or diseases involving cell death, has been identified.

### 3.1 Definitions

"Protective sequence", as used herein, refers to nucleic acid molecules comprising nucleic acid sequences which, when introduced into a cell predisposed to either undergo cell death or in the process of undergoing cell death, prevent, delay, or rescue the cell from death relative to a corresponding cell into which no exogenous protective nucleic acids have been introduced. In one embodiment, a protective sequence encodes a protective sequence product. In another embodiment, protective sequences are any transcriptional products of the sequences disclosed herein. In another embodiment, protective sequences comprise regulatory elements of the sequences disclosed herein which modulate the expression of a nucleic acid within a cell. For example, protective sequences, their products, or their regulatory elements may act to prevent, delay, or rescue a cell, cells, tissues, organs, or organisms from dying. Compounds which modulate protective sequence expression or activity of the protective sequence product can be used in the treatment of conditions, disorders or diseases associated with cell death processes. It is to be understood that the

protective sequences described above can act to ameliorate or delay symptoms related to cell death. Although the protective sequences may be involved directly in such cell death related conditions or disorders, in certain cases, the protective sequences will not normally be involved in such conditions or disorders, but will be effective for the treatment and/or prevention of such disorders. In these cases, modulation of the expression of the protective sequence and/or the activity of the protective sequence product will be useful for the treatment of conditions, disorders, or diseases involving cell death which are normally mediated by some other gene.

"Cell death", as used herein, refers to any mechanism and/or pathway whereby a cell undergoes a series of events which ultimately would lead to the death of the cell. For example, cell death may be caused by various processes including, but not limited to, apoptosis or programmed cell death, necrosis, or an as yet unidentified cell death pathway. Cell death may be induced in individual cells as a consequence of numerous internal and external stimuli including, but not limited to, genetic predisposition, toxic chemicals or processes, heat, cold, rapid environmental changes, radiation, viruses, prions, bacteria, disruption of nutrient balance, or exposure to bi-products and signaling from other cells undergoing cell death. The protective sequences disclosed herein, when introduced into a cell (*e.g.* a neuronal cell) which has undergone an event that would ultimately lead to cell death (*e.g.* ischemia), are capable of rescuing the cell from cell death. Moreover, when a protective sequence, in combination with a reporter gene (*e.g.* green fluorescent protein), is introduced into a cell which has undergone an event that would ultimately lead to cell death, expression of the reporter gene is an indication that the protective sequence is capable of rescuing the cell from cell death.

#### **4 BRIEF DESCRIPTION OF THE FIGURES**

Figures 1(A-J). Protective nucleic acids. See Table 1 for the identity, the sequence identifier number, the length in base pairs and the Accession Number for each of the sequences shown in these figures.

Figure 2. Restriction map and diagram of plasmid pCMV-SPORT2. This plasmid was used as the cloning vector for the protective sequences. Each clone was ligated

into the *SalI*-*NotI* restriction sites of the plasmid.

Figures 3(A- F). Protected Cortical Neurons Visualized by Detection of EGFP Expressing Cells. Figures 3A and 3B represent non-stroked, positive control samples. Figure 3C represents a positive control, stroked sample using Bcl-2. Figure 3D represents a stroked, negative control sample. Figure 3E represents a stroked sample protected by a representative protective sequence. Figure 3F presents the average number of neurons that survived for three days in both a stroked sample protected by a protective sequence and a corresponding stroked, negative control sample.

Figures 4(A-AB). Open Reading Frames for CNI-00718. This Figure depicts the 28 potential ORFs for CNI-00718. Also shown are the nucleotide sequences which encode the ORFs.

Figures 5(A-L). Open Reading Frames for CNI-00722. This Figure depicts the 12 potential ORFs for CNI-00722. Also shown are the nucleotide sequences which encode the ORFs.

Figures 6(A-K). Open Reading Frames for CNI-00725. This Figure depicts the 11 potential ORFs for CNI-00725. Also shown are the nucleotide sequences which encode the ORFs.

Figures 7(A-Z). Open Reading Frames for CNI-00726. This Figure depicts the 26 potential ORFs for CNI-00726. Also shown are the nucleotide sequences which encode the ORFs.

Figures 8(A-S). Open Reading Frames for CNI-00727. This Figure depicts the 19 potential ORFs for CNI-00727. Also shown are the nucleotide sequences which encode the ORFs.

Figures 9(A-X). Open Reading Frames for CNI-00728. This Figure depicts the 24 potential ORFs for CNI-00728. Also shown are the nucleotide sequences which encode the ORFs.

5                   Figures 10(A-V). Open Reading Frames for CNI-00729. This Figure depicts the 22 potential ORFs for CNI-00729. Also shown are the nucleotide sequences which encode the ORFs.

10                   Figures 11(A-I). Open Reading Frames for CNI-00730. This Figure depicts the 9 potential ORFs for CNI-00730. Also shown are the nucleotide sequences which encode the ORFs.

15                   Figures 12(A-G). Open Reading Frames for CNI-00731. This Figure depicts the 7 potential ORFs for CNI-00731. Also shown are the nucleotide sequences which encode the ORFs.

20                   Figures 13(A-H). Open Reading Frames for CNI-00732. This Figure depicts the 8 potential ORFs for CNI-00732. Also shown are the nucleotide sequences which encode the ORFs.

## 5                   **DETAILED DESCRIPTION OF THE INVENTION**

Protective sequences of the invention are described herein. Also described are recombinant, cloned and degenerate variants, homologs, orthologs, mutants and fragments thereof. The compositions of the invention further include protective sequence products (*e.g.* 25 proteins or RNA) which are encoded or produced by the nucleic acid molecules of the invention, and the modulation of protective sequence expression and/or gene product activity in the treatment of conditions, disorders, or diseases involving cell death. Further, antibodies directed against the protective sequence products, or conserved variants or fragments thereof, and viral-, cell-, plant-, and animal-based models by which the protective sequences may be 30 further characterized and utilized are also discussed in this section.



### 5.1 The Protective Sequences

The protective sequences of the invention are described in this section.

Specifically, these protective sequences have been shown to prevent, delay, or rescue cell death in a cell predisposed for undergoing cell death, whether the pathway that leads to the cell death involves apoptosis, necrosis or an as yet undefined pathway. The protective sequences, their SEQ ID NOS and additional information related to the protective sequences are listed below, in Table 1.

The protective sequences listed in Table 1 may be obtained using cloning methods well known to those skilled in the art, including but not limited to the use of appropriate probes to detect the protective sequences within an appropriate cDNA or gDNA (genomic DNA) library. (See, for example, Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratories, which is incorporated by reference herein in its entirety). Probes for the novel sequences reported herein may be obtained directly from CNI-NPP2-CP10, which represents a composite deposit containing the isolated clones, which was deposited with the ATCC as Accession No. PTA-1492 on March 16, 2000. Alternatively, oligonucleotide probes for the novel protective sequences may be synthesized based on the DNA sequences disclosed herein.

**TABLE 1**  
**PROTECTIVE SEQUENCES**

<u>Protective sequence</u>	<u>SEQ ID NO:</u>	<u>Figure No.</u>	<u>Length (bp)</u> <u>(NotI-SalI</u> <u>fragment)</u>
CNI-00718	1	1A	1794
CNI-00722	58	1B	810
CNI-00725	83	1C	920
CNI-00726	106	1D	2144
CNI-00727	159	1E	1293
CNI-00728	198	1F	1466
CNI-00729	247	1G	1659
CNI-00730	292	1H	722
CNI-00731	311	1I	364
CNI-00732	326	1J	1046

The isolated protective nucleic acid molecules of the invention include, in particular, nucleic acid molecules which comprise the following sequences: (a) nucleic acids of protective sequences, as well as allelic variants, homologs, mutants and fragments thereof; (b) nucleic acids which encode protective sequence products and/or their regulatory elements, or fragments thereof; (c) nucleic acids which encode fusion proteins comprising protective sequence products and/or their regulatory elements, or one or more protective sequence product domains and/or their regulatory elements fused to a heterologous polypeptide; (d) nucleic acids which hybridize to the above described sequences under highly stringent or moderately stringent conditions, including, but not limited to human homologs; and (e) complementary (*e.g.*, antisense) nucleic acids of the sequences described in (a) through (d), above. The nucleic acid molecules of the invention include, but are not limited to, cDNA, genomic DNA and RNA sequences.

The nucleic acids of the invention also include nucleic acids which have at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or more nucleic acid identity to the protective nucleic acids of (a)-(d) above. The nucleic acids of the invention further include nucleic acids which encode polypeptides having at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or higher amino acid sequence identity to the polypeptides encoded by the protective nucleic acids of (a)-(d).

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical overlapping positions/total # of positions x 100). In one embodiment, the two sequences are the same length.

The determination of percent identity between two sequences also can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a

mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleic acids homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25: 3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search that detects distant relationships between molecules (*Id.*). When utilizing BLAST, Gapped BLAST and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used (see <http://www.ncbi.nlm.nih.gov>). Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4 can be used.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted.

The nucleic acids of the invention further include: (a) any nucleic acid which hybridizes to a nucleic acid molecule of the invention under moderately stringent conditions, *e.g.*, hybridization to filter-bound DNA in 6x sodium chloride/sodium citrate (SSC) at about 45°C followed by one or more washes in 0.2xSSC/0.1% SDS at about 50-65°C, or (b) under highly stringent conditions, *e.g.*, hybridization to filter-bound nucleic acid in 6xSSC at about 45°C followed by one or more washes in 0.1xSSC/0.2% SDS at about 68°C, or under other hybridization conditions which are apparent to those of skill in the art (*see*, for example, Ausubel F.M. *et al.*, eds., 1989, *Current Protocols in Molecular Biology*, Vol. I, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York, at pp. 6.3.1-6.3.6 and

2.10.3). Preferably the nucleic acid molecule that hybridizes to the nucleic acid of (a) and (b), above, is one which comprises the complement of a nucleic acid molecule which encodes a protective sequence product. In a preferred embodiment, nucleic acid molecules comprising the nucleic acids of (a) and (b), above, encode protective sequence products.

Functionally equivalent protective sequence products include naturally occurring protective sequence products present in the same or different species. Functionally equivalent protective sequence products also include gene products which retain at least one of the biological activities of the protective sequence products, and/or which are recognized by and bind to antibodies (polyclonal or monoclonal) directed against the protective sequence products.

Among the nucleic acid molecules of the invention are deoxyoligonucleotides ("oligos") which hybridize under highly stringent or moderately stringent conditions to the nucleic acid molecules described above. In general, for probes between 14 and 70 nucleotides in length the melting temperature ( $T_m$ ) is calculated using the formula:  $T_m (^{\circ}\text{C}) = 81.5 + 16.6(\log[\text{monovalent cations (molar)}]) + 0.41 (\% \text{ G+C}) - (500/N)$  where  $N$  is the length of the probe. If the hybridization is carried out in a solution containing formamide, the melting temperature is calculated using the equation  $T_m (^{\circ}\text{C}) = 81.5 + 16.6(\log[\text{monovalent cations (molar)}]) + 0.41 (\% \text{ G+C}) - (0.61 \% \text{ formamide}) - (500/N)$  where  $N$  is the length of the probe. In general, hybridization is carried out at about 20-25 degrees below  $T_m$  (for DNA-DNA hybrids) or 10-15 degrees below  $T_m$  (for RNA-DNA hybrids).

Exemplary highly stringent conditions may refer, *e.g.*, to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C (for about 14-base oligos), 48°C (for about 17-base oligos), 55°C (for about 20-base oligos) and 60°C (for about 23-base oligos).

Fragments of the nucleic acid molecules can be at least 9 nucleotides in length. Fragments of the nucleic acid molecules can refer also to exons or introns, and, further, can refer to portions of coding regions that encode domains of protective sequence products.

The invention also encompasses (a) DNA vectors which contain any of the foregoing coding sequences and/or their complements (*i.e.*, antisense); (b) DNA expression vectors which contain any of the foregoing coding sequences operatively associated with a regulatory element which directs the expression of the coding sequences; and (c) genetically engineered host cells which contain such vectors or have been engineered to contain and/or

express a nucleic acid sequence of the invention, *e.g.*, any of the foregoing coding sequences operatively associated with a regulatory element which directs the expression of the coding sequences in the host cell. As used herein, regulatory elements include but are not limited to inducible and non-inducible promoters, enhancers, operators and other elements known to those skilled in the art which drive and regulate expression. The invention further includes fragments of any of the DNA sequences disclosed herein.

The nucleic acid molecules may encode or act as antisense molecules, useful, for example, in protective sequence regulation, and/or as hybridization probes and/or as primers in amplification reactions of protective nucleic acid sequences. Further, such sequences may be used as part of ribozyme and/or triple helix sequences, also useful for protective sequence regulation. Still further, such molecules may be used as components of diagnostic methods whereby, for example, the presence of a particular allele involved in a condition, disorder, or disease involving cell death may be detected.

The protective nucleic acids of the invention can be readily obtained, for example, by standard sequencing and the sequences provided herein.

As will be appreciated by those skilled in the art, DNA sequence polymorphisms of a protective sequence will exist within a population of individual organisms (*e.g.*, within a human population). Such polymorphisms may exist, for example, among individuals within a population due to natural allelic variation. Such polymorphisms include ones that lead to changes in amino acid sequence. An allele is one of a group of alternative forms of a gene that occur at a given genetic locus.

As used herein, the phrase "allelic variant" refers to a nucleic acid that occurs at a given locus or to a gene product encoded by that nucleic acid. Such natural allelic variations can typically result in 1-5% variance in the nucleic acid of a given gene.

Sequencing the gene of interest in a number of different individuals can identify alternative alleles. Using hybridization probes to identify the same genetic locus in a variety of individuals can readily carry this out.

As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising any of up to six open reading frames which may or may not encode a polypeptide of the invention. For example, the terms "gene" and "recombinant gene" refer to nucleic acid molecules encoding any of the open reading frames shown in Figures 4-13, and

described in Tables 2-11, respectively. The term can further include nucleic acid molecules comprising upstream and/or exon/intron sequences and structures.

**TABLE 2****OPEN READING FRAMES FOR CNI-00718**

OPEN READING FRAME NUMBER	LENGTH	LOCATION	SEQUENCE ID. NO.
1	39 Nucleotide	202-240 of Seq. Id. No. 1	2
	12 Amino Acid		3
2	45 Nucleotide	315-359 of Seq. Id. No. 1	4
	14 Amino Acid		5
3	51 Nucleotide	356-406 of Seq. Id. No. 1	6
	16 Amino Acid		7
4	42 Nucleotide	385-426 of Seq. Id. No. 1	8
	13 Amino Acid		9
5	15 Nucleotide	423-437 of Seq. Id. No. 1	10
	4 Amino Acids		11
6	12 Nucleotide	467-478 of Seq. Id. No. 1	12
	3 Amino Acid		13
7	27 Nucleotide	483-509 of Seq. Id. No. 1	14
	8 Amino Acid		15
8	51 Nucleotide	597-647 of Seq. Id. No. 1	16
	16 Amino Acid		17
9	30 Nucleotide	685-714 of Seq. Id. No. 1	18
	9 Amino Acids		19
10	221 Nucleotide	704-925 of Seq. Id. No. 1	20
	73 Amino Acid		21
11	69 Nucleotide	715-783 of Seq. Id. No. 1	22
	22 Amino Acid		23
12	57 Nucleotide	727-783 of Seq. Id. No. 1	24
	18 Amino Acid		25
13	18 Nucleotide	735-752 of Seq. Id. No. 1	26
	5 Amino Acids		27
14	30 Nucleotide	891-920 of Seq. Id. No. 1	28
	9 Amino Acid		29
15	339 Nucleotide	954-1292 of Seq. Id. No. 1	30
	112 Amino Acid		31
16	63 Nucleotide	997-1059 of Seq. Id. No. 1	32
	20 Amino Acid		33
17	207 Nucleotide	1086-1292 of Seq. Id. No. 1	34
	68 Amino Acids		35
18	72 Nucleotide	1221-1292 of Seq. Id. No. 1	36
	23 Amino Acid		37
19	24 Nucleotide	1335-1358 of Seq. Id. No. 1	38
	7 Amino Acid		39

20	21 Nucleotide	1367-1387 of Seq. Id. No. 1	40
	6 Amino Acid		41
21	36 Nucleotide	1439-1474 of Seq. Id. No. 1	42
	11 Amino Acids		43
22	183 Nucleotide	1461-1643 of Seq. Id. No. 1	44
	60 Amino Acid		45
23	99 Nucleotide	1541-1639 of Seq. Id. No. 1	46
	32 Amino Acid		47
24	18 Nucleotide	1626-1643 of Seq. Id. No. 1	48
	5 Amino Acid		49
25	12 Nucleotide	1632-1643 of Seq. Id. No. 1	50
	3 Amino Acids		51
26	21 Nucleotide	1684-1704 of Seq. Id. No. 1	52
	6 Amino Acid		53
27	18 Nucleotide	1725-1742 of Seq. Id. No. 1	54
	5 Amino Acids		55
28	27 Nucleotide	1747-1773 of Seq. Id. No. 1	56
	8 Amino Acids		57



**TABLE 3****OPEN READING FRAMES FOR CNI-00722**

5	OPEN READING FRAME NUMBER	LENGTH	LOCATION	SEQUENCE ID. NO.
10	1	15 Nucleotide	242-256 of Seq. Id. No. 58	59
		4 Amino Acid		60
	2	27 Nucleotide	301-327 of Seq. Id. No. 58	61
		8 Amino Acid		62
	3	12 Nucleotide	316-327 of Seq. Id. No. 58	63
		3 Amino Acid		64
15	4	51 Nucleotide	385-435 of Seq. Id. No. 58	65
		16 Amino Acid		66
	5	33 Nucleotide	446-478 of Seq. Id. No. 58	67
		10 Amino Acid		68
20	6	15 Nucleotide	478-492 of Seq. Id. No. 58	69
		4 Amino Acid		70
	7	135 Nucleotide	498-632 of Seq. Id. No. 58	71
		44 Amino Acid		72
	8	57 Nucleotide	576-632 of Seq. Id. No. 58	73
		18 Amino Acid		74
25	9	96 Nucleotide	632-727 of Seq. Id. No. 58	75
		31 Amino Acid		76
	10	93 Nucleotide	635-727 of Seq. Id. No. 58	77
		30 Amino Acid		78
30	11	51 Nucleotide	714-764 of Seq. Id. No. 58	79
		16 Amino Acids		80
	12	57 Nucleotide	754-810 of Seq. Id. No. 58	81
		19 Amino Acids		82

**TABLE 4****OPEN READING FRAMES FOR CNI-00725**

5	OPEN READING FRAME NUMBER	LENGTH	LOCATION	SEQUENCE ID. NO.
10	1	21 Nucleotide	67-87 of Seq. Id. No. 83	84
		6 Amino Acid		85
	2	39 Nucleotide	187-225 of Seq. Id. No. 83	86
		12 Amino Acid		87
	3	48 Nucleotide	258-305 of Seq. Id. No. 83	88
		15 Amino Acid		89
15	4	75 Nucleotide	262-336 of Seq. Id. No. 83	90
		24 Amino Acid		91
	5	99 Nucleotide	333-431 of Seq. Id. No. 83	92
		32 Amino Acids		93
20	6	12 Nucleotide	359-370 of Seq. Id. No. 83	94
		3 Amino Acid		95
	7	54 Nucleotide	378-431 of Seq. Id. No. 83	96
		17 Amino Acid		97
	8	45 Nucleotide	482-526 of Seq. Id. No. 83	98
		14 Amino Acids		99
25	9	63 Nucleotide	619-681 of Seq. Id. No. 83	100
		20 Amino Acid		101
	10	42 Nucleotide	640-681 of Seq. Id. No. 83	102
		13 Amino Acids		103
30	11	116 Nucleotide	805-920 of Seq. Id. No. 83	104
		38 Amino Acids		105

**TABLE 5****OPEN READING FRAMES FOR CNI-00726**

OPEN READING FRAME NUMBER	LENGTH	LOCATION	SEQUENCE ID. NO.
1	444 Nucleotide	23-466 of Seq. Id. No. 106	107
	147 Amino Acid		108
2	24 Nucleotide	111-134 of Seq. Id. No. 106	109
	7 Amino Acid		110
3	15 Nucleotide	138-152 of Seq. Id. No. 106	111
	4 Amino Acid		112
4	318 Nucleotide	149-466 of Seq. Id. No. 106	113
	105 Amino Acid		114
5	42 Nucleotide	163-204 of Seq. Id. No. 106	115
	13 Amino Acids		116
6	294 Nucleotide	173-466 of Seq. Id. No. 106	117
	97 Amino Acid		118
7	30 Nucleotide	201-230 of Seq. Id. No. 106	119
	9 Amino Acid		120
8	12 Nucleotide	232-243 of Seq. Id. No. 106	121
	3 Amino Acid		122
9	177 Nucleotide	290-466 of Seq. Id. No. 106	123
	58 Amino Acids		124
10	36 Nucleotide	312-347 of Seq. Id. No. 106	125
	11 Amino Acids		126
11	18 Nucleotide	352-369 of Seq. Id. No. 106	127
	5 Amino Acid		128
12	63 Nucleotide	404-466 of Seq. Id. No. 106	129
	20 Amino Acid		130
13	60 Nucleotide	407-466 of Seq. Id. No. 106	131
	19 Amino Acid		132
14	45 Nucleotide	422-466 of Seq. Id. No. 106	133
	14 Amino Acids		134
15	27 Nucleotide	624-650 of Seq. Id. No. 106	135
	8 Amino Acids		136
16	72 Nucleotide	1006-1077 of Seq. Id. No. 106	137
	23 Amino Acid		138
17	57 Nucleotide	1224-1280 of Seq. Id. No. 106	139
	18 Amino Acid		140
18	48 Nucleotide	1335-1382 of Seq. Id. No. 106	141
	15 Amino Acid		142

19	15 Nucleotide	1382-1396 of Seq. Id. No. 106	143
	4 Amino Acids		144
20	78 Nucleotide	1492-1569 of Seq. Id. No. 106	145
	25 Amino Acid		146
21	33 Nucleotide	1514-1546 of Seq. Id. No. 106	147
	10 Amino Acid		148
22	156 Nucleotide	1670-1825 of Seq. Id. No. 106	149
	51 Amino Acid		150
23	30 Nucleotide	1819-1848 of Seq. Id. No. 106	151
	9 Amino Acids		152
24	69 Nucleotide	1827-1895 of Seq. Id. No. 106	153
	22 Amino Acids		154
25	63 Nucleotide	1833-1895 of Seq. Id. No. 106	155
	20 Amino Acids		156
26	66 Nucleotide	1951-2016 of Seq. Id. No. 106	157
	21 Amino Acids		158

**TABLE 6****OPEN READING FRAMES FOR CNI-00727**

OPEN READING FRAME NUMBER	LENGTH	LOCATION	SEQUENCE ID. NO.
1	45 Nucleotide	237-281 of Seq. Id. No. 159	160
	14 Amino Acid		161
2	27 Nucleotide	255-281 of Seq. Id. No. 159	162
	8 Amino Acid		163
3	12 Nucleotide	395-406 of Seq. Id. No. 159	164
	3 Amino Acid		165
4	45 Nucleotide	403-447 of Seq. Id. No. 159	166
	14 Amino Acid		167
5	48 Nucleotide	419-466 of Seq. Id. No. 159	168
	15 Amino Acids		169
6	27 Nucleotide	454-480 of Seq. Id. No. 159	170
	8 Amino Acid		171
7	39 Nucleotide	610-648 of Seq. Id. No. 159	172
	12 Amino Acid		173
8	165 Nucleotide	658-822 of Seq. Id. No. 159	174
	54 Amino Acid		175
9	132 Nucleotide	691-822 of Seq. Id. No. 159	176
	43 Amino Acids		177
10	123 Nucleotide	700-822 of Seq. Id. No. 159	178
	40 Amino Acid		179
11	111 Nucleotide	712-822 of Seq. Id. No. 159	180
	36 Amino Acid		181
12	57 Nucleotide	945-1001 of Seq. Id. No. 159	182
	18 Amino Acid		183
13	18 Nucleotide	952-969 of Seq. Id. No. 159	184
	5 Amino Acids		185
14	15 Nucleotide	962-976 of Seq. Id. No. 159	186
	4 Amino Acid		187
15	99 Nucleotide	973-1071 of Seq. Id. No. 159	188
	32 Amino Acid		189
16	12 Nucleotide	1071-1082 of Seq. Id. No. 159	190
	3 Amino Acid		191
17	63 Nucleotide	1131-1193 of Seq. Id. No. 159	192
	20 Amino Acid		193
18	42 Nucleotide	1152-1193 of Seq. Id. No. 159	194
	13 Amino Acids		195
19	12 Nucleotide	1165-1176 of Seq. Id. No. 159	196
	3 Amino Acids		197

TABLE 7

OPEN READING FRAMES FOR CNI-00728

OPEN READING FRAME NUMBER	LENGTH	LOCATION	SEQUENCE ID. NO.
1	129 Nucleotide	30-158 of Seq. Id. No. 198	199
	42 Amino Acid		200
2	69 Nucleotide	70-138 of Seq. Id. No. 198	201
	22 Amino Acid		202
3	42 Nucleotide	117-158 of Seq. Id. No. 198	203
	13 Amino Acid		204
4	39 Nucleotide	187-225 of Seq. Id. No. 198	205
	12 Amino Acid		206
5	33 Nucleotide	193-225 of Seq. Id. No. 198	207
	10 Amino Acid		208
6	24 Nucleotide	202-225 of Seq. Id. No. 198	209
	7 Amino Acid		210
7	15 Nucleotide	225-239 of Seq. Id. No. 198	211
	4 Amino Acid		212
8	21 Nucleotide	331-351 of Seq. Id. No. 198	213
	6 Amino Acid		214
9	42 Nucleotide	384-425 of Seq. Id. No. 198	215
	13 Amino Acid		216
10	60 Nucleotide	404-463 of Seq. Id. No. 198	217
	19 Amino Acid		218
11	15 Nucleotide	536-550 of Seq. Id. No. 198	219
	4 Amino Acid		220
12	39 Nucleotide	626-664 of Seq. Id. No. 198	221
	12 Amino Acid		222
13	102 Nucleotide	689-790 of Seq. Id. No. 198	223
	33 Amino Acid		224
14	60 Nucleotide	731-790 of Seq. Id. No. 198	225
	19 Amino Acid		226
15	87 Nucleotide	738-824 of Seq. Id. No. 198	227
	28 Amino Acid		228
16	180 Nucleotide	910-1089 of Seq. Id. No. 198	229
	59 Amino Acid		230
17	99 Nucleotide	991-1089 of Seq. Id. No. 198	231
	32 Amino Acid		232
18	27 Nucleotide	1063-1089 of Seq. Id. No. 198	233
	8 Amino Acid		234

19	150 Nucleotide	1124-1273 of Seq. Id. No. 198	235
	49 Amino Acid		236
20	54 Nucleotide	1143-1196 of Seq. Id. No. 198	237
	17 Amino Acid		238
21	87 Nucleotide	1187-1273 of Seq. Id. No. 198	239
	28 Amino Acid		240
22	42 Nucleotide	1242-1283 of Seq. Id. No. 198	241
	13 Amino Acid		242
23	15 Nucleotide	1306-1320 of Seq. Id. No. 198	243
	4 Amino Acids		244
24	139 Nucleotide	1382-1466 of Seq. Id. No. 198	245
	46 Amino Acids		246

**TABLE 8**  
**OPEN READING FRAMES FOR CNI-00729**

OPEN READING FRAME NUMBER	LENGTH	LOCATION	SEQUENCE ID. NO.
1	1386 Nucleotide	140-1525 of Seq. Id. No. 247	248
	461 Amino Acid		249
2	75 Nucleotide	213-287 of Seq. Id. No. 247	250
	24 Amino Acid		251
3	69 Nucleotide	219-287 of Seq. Id. No. 247	252
	22 Amino Acid		253
4	39 Nucleotide	357-395 of Seq. Id. No. 247	254
	12 Amino Acid		255
5	72 Nucleotide	417-488 of Seq. Id. No. 247	256
	23 Amino Acid		257
6	1068 Nucleotide	458-1525 of Seq. Id. No. 247	258
	355 Amino Acid		259
7	12 Nucleotide	477-488 of Seq. Id. No. 247	260
	3 Amino Acid		261
8	1038 Nucleotide	488-1525 of Seq. Id. No. 247	262
	345 Amino Acid		263
9	918 Nucleotide	608-1525 of Seq. Id. No. 247	264
	305 Amino Acid		265
10	888 Nucleotide	638-1525 of Seq. Id. No. 247	266
	295 Amino Acid		267
11	75 Nucleotide	699-773 of Seq. Id. No. 247	268
	24 Amino Acid		269
12	663 Nucleotide	863-1525 of Seq. Id. No. 247	270
	220 Amino Acid		271
13	462 Nucleotide	1064-1525 of Seq. Id. No. 247	272
	153 Amino Acid		273
14	432 Nucleotide	1094-1525 of Seq. Id. No. 247	274
	143 Amino Acid		275
15	423 Nucleotide	1103-1525 of Seq. Id. No. 247	276
	140 Amino Acid		277
16	339 Nucleotide	1187-1525 of Seq. Id. No. 247	278
	112 Amino Acid		279
17	63 Nucleotide	1290-1352 of Seq. Id. No. 247	280
	20 Amino Acid		281
18	33 Nucleotide	1320-1352 of Seq. Id. No. 247	282
	10 Amino Acid		283
19	238 Nucleotide	1422-1659 of Seq. Id. No. 247	284
	79 Amino Acid		285



20	78 Nucleotide	1448-1525 of Seq. Id. No. 247	286
	25 Amino Acid		287
21	67 Nucleotide	1593-1659 of Seq. Id. No. 247	288
	22 Amino Acids		289
22	41 Nucleotide	1619-1659 of Seq. Id. No. 247	290
	13 Amino Acids		291

**TABLE 9****OPEN READING FRAMES FOR CNI-00730**

5	OPEN READING FRAME NUMBER	LENGTH	LOCATION	SEQUENCE ID. NO.
10	1	429 Nucleotide	128-556 of Seq. Id. No. 292	293
		142 Amino Acid		294
	2	30 Nucleotide	264-293 of Seq. Id. No. 292	295
		9 Amino Acid		296
	3	18 Nucleotide	276-293 of Seq. Id. No. 292	297
		5 Amino Acid		298
15	4	21 Nucleotide	435-455 of Seq. Id. No. 292	299
		6 Amino Acid		300
	5	51 Nucleotide	474-524 of Seq. Id. No. 292	301
		16 Amino Acids		302
20	6	51 Nucleotide	506-556 of Seq. Id. No. 292	303
		16 Amino Acid		304
	7	33 Nucleotide	524-556 of Seq. Id. No. 292	305
		10 Amino Acid		306
	8	51 Nucleotide	573-623 of Seq. Id. No. 292	307
		16 Amino Acid		308
25	9	74 Nucleotide	649-722 of Seq. Id. No. 292	309
		24 Amino Acids		310

**TABLE 10****OPEN READING FRAMES FOR CNI-00731**

5	OPEN READING FRAME NUMBER	LENGTH	LOCATION	SEQUENCE ID. NO.
10	1	48 Nucleotide	56-103 of Seq. Id. No. 311	312
		15 Amino Acid		313
	2	24 Nucleotide	80-103 of Seq. Id. No. 311	314
		7 Amino Acid		315
15	3	18 Nucleotide	86-103 of Seq. Id. No. 311	316
		5 Amino Acid		317
	4	99 Nucleotide	107-205 of Seq. Id. No. 311	318
		32 Amino Acid		319
20	5	72 Nucleotide	199-270 of Seq. Id. No. 311	320
		23 Amino Acids		321
	6	36 Nucleotide	235-270 of Seq. Id. No. 311	322
		11 Amino Acid		323
	7	98 Nucleotide	267-364 of Seq. Id. No. 311	324
		32 Amino Acids		325

TABLE 11OPEN READING FRAMES FOR CNI-00732

OPEN READING FRAME NUMBER	LENGTH	LOCATION	SEQUENCE ID. NO.
1	24 Nucleotide	23-46 of Seq. Id. No. 326	327
	7 Amino Acid		328
2	63 Nucleotide	100-162 of Seq. Id. No. 326	329
	20 Amino Acid		330
3	108 Nucleotide	418-525 of Seq. Id. No. 326	331
	35 Amino Acid		332
4	18 Nucleotide	611-628 of Seq. Id. No. 326	333
	5 Amino Acid		334
5	51 Nucleotide	671-721 of Seq. Id. No. 326	335
	16 Amino Acids		336
6	36 Nucleotide	686-721 of Seq. Id. No. 326	337
	11 Amino Acid		338
7	30 Nucleotide	727-756 of Seq. Id. No. 326	339
	9 Amino Acid		340
8	152 Nucleotide	895-1046 of Seq. Id. No. 326	341
	50 Amino Acids		342

Alternative or differential splicing of a gene that encodes any of the open reading frames shown in Figures 4-13 can also generate an alternative or differential protective sequence product. For example, a gene that generates one of the protective sequence products shown in Figures 4-13 may be encoded by 4 out of 6 exons that comprise the entire gene; alternative or differential splicing of the gene can generate other protective sequence products that are encoded by 1, 2, 3, 4, 5, or 6 of the exons in the gene (Lewin, 2000, Genes VII, Oxford University Press, 702-705). The present invention also includes nucleic acid molecules comprising nucleic acids that separately encode these alternative or differential protective sequence products.

In a specific embodiment, the nucleic acid molecules comprise nucleic acids that encode an open reading frame of at least 3 contiguous amino acid residues from a full-length protein. In alternate embodiments, the nucleic acid molecules comprise an open reading frame which encodes at least about 5, 8, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450 or more contiguous amino acid residues of a protein.

The sequence obtained from clones containing partial coding sequences or non-coding sequences can be used to obtain the entire coding region by using the RACE method, for example (Chenchik, et al., 1995, CLONTECHniques (X) 1: 5-8; Barnes, 1994, Proc. Natl. Acad. Sci. USA 91: 2216-2220; and Cheng et al., Proc. Natl. Acad. Sci. USA 91: 5695-5699). Oligonucleotides can be designed based on the sequence obtained from the partial clone that can amplify a reverse transcribed mRNA encoding the entire coding sequence. Alternatively, probes can be used to screen cDNA libraries prepared from an appropriate cell or cell line in which the protective sequence is transcribed.

With respect to allelic variants of protective sequences associated with a condition, disorder, or disease involving cell death, any and all such nucleotide variations and resulting amino acid polymorphisms or variations which are the result of natural allelic variation of the protective sequence are intended to be within the scope of the present invention. Such allelic variants include, but are not limited to, ones that do not alter the functional activity of the protective sequence product.

With respect to the cloning of additional allelic variants of the isolated protective sequence and homologues and orthologs from other species (*e.g.*, guinea pig, cow, mouse), the isolated protective sequences disclosed herein may be labeled and used to screen

a cDNA library constructed from mRNA obtained from appropriate cells or tissues (*e.g.*, brain) derived from the organism (*e.g.*, guinea pig, cow and mouse) of interest. The hybridization conditions used generally should be of a lower stringency when the cDNA library is derived from an organism different from the type of organism from which the labeled sequence was derived, and can routinely be determined based on, *e.g.*, relative relatedness of the target and reference organisms.

Alternatively, the labeled fragment may be used to screen a genomic library derived from the organism of interest, again, using appropriately stringent conditions. Appropriate stringency conditions are well known to those of skill in the art as discussed above, and will vary predictably depending on the specific organisms from which the library and the labeled sequences are derived. For guidance regarding such conditions, *see*, for example, Sambrook, *et al.*, 1989, *Molecular Cloning, A Laboratory Manual, Second Edition*, Cold Spring Harbor Press, N.Y.; and Ausubel, *et al.*, 1989-1999, *Current Protocols in Molecular Biology*, Green Publishing Associates and Wiley Interscience, N.Y., both of which are incorporated herein by reference in their entirety.

Additionally, the cloning of homologs and orthologs of the isolated protective sequence from other species (*e.g.* mouse) could also occur using the knowledge of syntenic regions and/or genes. Syntenic genes are genes which are believed to be located on the same chromosome because they are lost along with a marker gene which is known to be located on that chromosome. There are well-established genetic maps of specific chromosome regions that show syntenic regions between chromosomes of humans and other species that can be utilized, by one skilled in the art, for this purpose.

Further, a protective sequence allelic variant may be isolated from, for example, human nucleic acid, by performing PCR using two degenerate oligonucleotide primer pools designed on the basis of amino acid sequences within the protective sequence product of interest. The template for the reaction may be cDNA obtained by reverse transcription of mRNA prepared from, for example, human or non-human cell lines or tissue known or suspected to express a wild type or mutant protective sequence allele. In one embodiment, the allelic variant is isolated from an individual who has a condition, disorder, or disease involving cell death. Such variants are described in the examples below.

The PCR product may be subcloned and sequenced to ensure that the amplified sequences represent the sequences of a protective nucleic acid sequence. The PCR fragment may then be used to isolate a full-length cDNA clone by a variety of methods. For example, the amplified fragment may be labeled and used to screen a bacteriophage cDNA library. Alternatively, the labeled fragment may be used to isolate genomic clones via the screening of a genomic library.

PCR technology also may be utilized to isolate full-length cDNA sequences. For example, RNA may be isolated, following standard procedures, from an appropriate cellular or tissue source. A reverse transcription reaction may be performed on the RNA using an oligonucleotide primer specific for the most 5' end of the amplified fragment for the priming of first strand synthesis. The resulting RNA/DNA hybrid may then be "tailed" with guanines using a standard terminal transferase reaction. The hybrid may be digested with RNAase H and second strand synthesis may then be primed with a poly-C primer. Thus, cDNA sequences upstream of the amplified fragment may easily be isolated. For a review of cloning strategies which may be used, see *e.g.*, Sambrook *et al.*, 1989, *supra*, or Ausubel *et al.*, *supra*.

In cases where the isolated protective sequence is the normal, or wild type gene, this gene may be used to isolate mutant alleles of the protective sequence. Such an isolation is preferable in processes and disorders that are known or suspected to have a genetic basis. Mutant alleles may be isolated from individuals either known or suspected to have a genotype which contributes to symptoms of conditions, disorders, or diseases involving cell death. Mutant alleles and mutant allele products may then be utilized in the therapeutic and diagnostic assay systems described below.

A cDNA of the mutant protective sequence may be isolated, for example, by using PCR, a technique well known to those of skill in the art. In this case, the first cDNA strand may be synthesized by hybridizing an oligo-dT oligonucleotide to mRNA isolated from tissue known or suspected to be expressed in an individual putatively carrying the mutant allele, and by extending the new strand with reverse transcriptase. The second strand of the cDNA is then synthesized using an oligonucleotide that hybridizes specifically to the 5' end of the normal protective sequence. Using these two primers, the product is then amplified via PCR, cloned into a suitable vector and subjected to DNA sequence analysis

through methods well known to those of skill in the art. By comparing the DNA sequence of the mutant protective sequence to that of the normal protective sequence, the mutation(s) responsible for the loss or alteration of function of the mutant gene product can be ascertained.

5                   Alternatively, a genomic or cDNA library can be constructed and screened using DNA or RNA, respectively, from a tissue known to or suspected of expressing the protective sequence of interest in an individual suspected of or known to carry the mutant allele. The normal protective sequence or any suitable fragment thereof may then be labeled and used as a probe to identify the corresponding mutant allele in the library. The clone  
10                   containing this protective sequence may then be purified through methods routinely practiced in the art, and subjected to sequence analysis as described above in this Section.

                  Additionally, an expression library can be constructed utilizing DNA isolated from or cDNA synthesized from a tissue known to or suspected of expressing the protective sequence of interest in an individual suspected of or known to carry the mutant allele. In this  
15                   manner, protective sequence products made by the tissue containing the putative mutant alleles may be expressed and screened using standard antibody screening techniques in conjunction with antibodies raised against the normal protective sequence product, as described, below, in Section 5.3 (For screening techniques, see, for example, Harlow, E. and Lane, eds., 1988, "Antibodies: A Laboratory Manual", Cold Spring Harbor Press, Cold Spring  
20                   Harbor.) In cases where the mutation results in an expressed protective sequence product with altered function (*e.g.*, as a result of a missense mutation), a polyclonal set of antibodies are likely to cross-react with the mutant protective sequence product. Library clones detected via their reaction with such labeled antibodies can be purified and subjected to sequence analysis as described in this Section, above.

25                   The invention also includes nucleic acid molecules, preferably DNA molecules that are the complements of the nucleic acids of the preceding paragraphs.

                  In certain embodiments, the protective nucleic acid molecules of the invention are present as part of protective nucleic acid molecules comprising nucleic acid sequences which do not contain heterologous (*e.g.*, cloning vector or expression vector) sequences. In  
30                   other embodiments, the protective nucleic acid molecules of the invention further comprise vector sequences, *e.g.*, cloning vectors or expression vectors.



## 5.2 Protein Products of the Protective Sequences

Protective sequence products or fragments thereof of the invention can be prepared for a variety of uses, including but not limited to, prophylactic or therapeutic modulators of protective sequence product function, for the generation of antibodies, diagnostic assays, or for the identification of other cellular or extracellular protective sequence products involved in the regulation of conditions, disorders, or diseases involving cell death.

The protective sequence products of the invention include, but are not limited to, human protective sequence products and non-human protective sequence products, *e.g.*, mammalian (such as bovine or guinea pig), protective sequence products.

Protective sequence products of the invention, sometimes referred to herein as a "protective sequence protein" or "protective sequence polypeptide," includes those gene products encoded by any of up to six translational reading frames of the protective sequence sequences depicted in Table 1, as well as gene products encoded by other human allelic variants and non-human variants of protective sequence products which can be identified by the methods herein described. Among such protective sequence product variants are protective sequence products comprising amino acid residues encoded by polymorphisms of such protective sequence products.

In addition, protective sequence products of the invention may include proteins that represent functionally equivalent gene products. Functionally equivalent protective sequence products may include, for example, protective sequence products encoded by one of the nucleic acid molecules described in Section 5.1, above. In preferred embodiments, such functionally equivalent protective sequence products are naturally occurring gene products. Functionally equivalent protective sequence products also include gene products which retain at least one of the biological activities of the protective sequence products described above, and/or which are recognized by and bind to antibodies (polyclonal or monoclonal) directed against protective sequence products of the invention.

Equivalent protective sequence products may contain deletions, including internal deletions, additions, including additions yielding fusion proteins, or substitutions of amino acid residues within and/or adjacent to the amino acid sequence encoded by the protective sequence sequences described, above, in Section 5.1. Generally, deletions will be

deletions of single amino acid residues, or deletions of no more than about 2, 3, 4, 5, 10 or 20 amino acid residues, either contiguous or non-contiguous. Generally, additions or substitutions, other than additions which yield fusion proteins, will be additions or substitutions of single amino acid residues, or additions or substitutions of no more than about 2, 3, 4, 5, 10 or 20 amino acid residues, either contiguous or non-contiguous. Preferably, these modifications result in a "silent" change, in that the change produces a protective sequence product with the same activity as the original protective sequence product. However, nucleic acid changes resulting in amino acid additions or substitutions may also be made for the purpose of modifying the protective sequence product in order to generally enhance their use as therapeutic agents or components for assays, such modifications to include, but not be limited to, stabilizing the product against degradation, enhancing pharmacokinetic properties, modifying site tropisms at the level of cells, tissues, organs, or organisms.

Amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine and glutamine; positively charged (basic) amino acids include arginine, lysine and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Additionally, non-natural amino acids, including, but not limited to, D-amino acids may be used.

Alternatively, where alteration of function is desired, addition(s), deletion(s) or non-conservative alterations can produce altered, including reduced-activity, protective sequence products. Such alterations can, for example, alter one or more of the biological functions of the protective sequence product. Further, such alterations can be selected so as to generate protective sequence products which include, but are not limited to, products which are better suited for expression, scale up, *etc.* in the host cells chosen. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

Protective sequence products of the invention also include gene products generated by alternative or differential splicing patterns of a gene that encodes for the

peptides shown in Figures 4-13. An isolated gene often includes alternating exons and introns; as a result, the same gene can generate a variety of gene products by alternative or differential forms of splicing.

Protein fragments and/or peptides of the invention may comprise at least as many contiguous amino acid residues as necessary to represent an epitope fragment (that is to be recognized by an antibody directed to the protein). Examples of such protein fragments and/or peptides of the invention are shown by the open reading frames of the protective sequences shown in Figures 4-13, and described in Tables 2-11, respectively. In one nonlimiting embodiment of the invention, such protein fragments or peptides comprise at least about 3 contiguous amino acid residues from a full-length protein. In alternate embodiments, the protein fragments and peptides of the invention can comprise about 5, 8, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450 or more contiguous amino acid residues of a protein.

Peptides and/or proteins corresponding to one or more domains of the protein as well as fusion proteins in which a protein, or a portion of a protein such as a truncated protein or peptide or a protein domain, is fused to an unrelated protein are also within the scope of this invention. Such proteins and peptides can be designed on the basis of the nucleic acids disclosed in Section 5.1, above. Fusion proteins include, but are not limited to, IgFc fusions which stabilize the protein or peptide and prolong half-life *in vivo*; or fusions to any amino acid sequence which allows the fusion protein to be anchored to the cell membrane; or fusions to an enzyme, fluorescent protein, luminescent protein or a epitope tagged protein or peptide which provides a marker function.

The protein sequences described above can include a domain, which comprises a protein transduction domain which targets the protective sequence product for delivery to various tissues and more particularly across the brain blood barrier, using, for example, the protein transduction domain of human immunodeficiency virus TAT protein (Schwarze *et al.*, 1999, Science 285: 1569-72).

The protein sequences described above can include a domain, which comprises a signal sequence that targets the gene product for secretion. As used herein, a signal sequence includes a peptide of at least about 15 or 20 amino acid residues in length which occurs at the N-terminus of secretory and membrane-bound proteins and which

contains at least about 70% hydrophobic amino acid residues such as alanine, leucine, isoleucine, phenylalanine, proline, tyrosine, tryptophan or valine. In a preferred embodiment, a signal sequence contains at least about 10 to 40 amino acid residues, preferably about 19-34 amino acid residues and has at least about 60-80%, more preferably 65-75% and more  
5 preferably at least about 70% hydrophobic residues. A signal sequence serves to direct a protein containing such a sequence to a lipid bilayer.

A signal sequence of a polypeptide of the invention can be used to facilitate secretion and isolation of the secreted protein or other proteins of interest. Signal sequences are typically characterized by a core of hydrophobic amino acids, which are generally cleaved  
10 from the mature protein during secretion in one or more cleavage events. Such signal peptides contain processing sites that allow cleavage of the signal sequence from the mature proteins as they pass through the secretory pathway. Thus, the invention pertains to the described polypeptides having a signal sequence (that is, "immature" polypeptides), as well as to the signal sequences themselves and to the polypeptides in the absence of a signal sequence  
15 (*i.e.*, the "mature" cleavage products). It is to be understood that polypeptides of the invention can further comprise polypeptides comprising any signal sequence having characteristics as described above and a mature polypeptide sequence.

In one embodiment, a nucleic acid sequence encoding a signal sequence of the invention can be operably linked in an expression vector to a protein of interest, such as a  
20 protein which is ordinarily not secreted or is otherwise difficult to isolate. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is subsequently or concurrently cleaved. The protein can then be readily purified from the extracellular medium by art recognized methods. Alternatively, the signal sequence can be linked to the protein of  
25 interest using a sequence which facilitates purification, such as with a GST domain.

Finally, the proteins of the invention also include protein sequences wherein domains encoded by any transcriptional or post-transcriptional, and/or translational or post-translational modifications, or fragments thereof, have been deleted. The polypeptides of the invention can further comprise posttranslational modifications, including, but not limited to  
30 glycosylations, acetylations and myrisalations.

The protective sequence products, peptide fragments thereof and fusion proteins thereof may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing the protective sequence products, polypeptides, peptides, fusion peptide and fusion polypeptides of the invention by expressing  
5 nucleic acid containing protective sequence sequences are described herein. Methods that are well known to those skilled in the art can be used to construct expression vectors containing protective sequence product coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* genetic recombination. See, for example, the  
10 techniques described in Sambrook, *et al.*, 1989, *supra*, and Ausubel, *et al.*, 1989, *supra*. Alternatively, RNA capable of encoding protective sequence product sequences may be chemically synthesized using, for example, synthesizers. See, for example, the techniques described in "Oligonucleotide Synthesis", 1984, Gait, ed., IRL Press, Oxford.

A variety of host-expression vector systems may be utilized to express the  
15 protective sequence product coding sequences of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, exhibit the protective sequence product of the invention *in situ*. These include, but are not limited to, microorganisms such as bacteria  
20 (*e.g.*, *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing protective sequence product coding sequences; yeast (*e.g.*, *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing the protective sequence product coding sequences; insect cell systems infected with recombinant virus expression vectors (*e.g.*, baculovirus) containing the protective  
25 sequence product coding sequences; plant cell systems infected with recombinant virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (*e.g.*, Ti plasmid) containing protective sequence product coding sequences; or mammalian cell systems (*e.g.*, COS, CHO, BHK, 293, 3T3) harboring recombinant expression constructs containing promoters derived  
30 from the genome of mammalian cells (*e.g.*, metallothioneine promoter) or from mammalian viruses (*e.g.*, the adenovirus late promoter; the vaccinia virus 7.5K promoter).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the protective sequence product being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of protective sequence product or for raising  
5 antibodies to protective sequence product, for example, vectors which direct the expression of high levels of fusion protein products which are readily purified may be desirable. Such vectors include, but are not limited to, the *E. coli* expression vector pUR278 (Ruther *et al.*, 1983, EMBO J. 2:1791), in which the protective sequence product coding sequence may be ligated individually into the vector in frame with the *lacZ* coding region so that a fusion  
10 protein is produced; pIN vectors (Inouye and Inouye, 1985, Nucleic Acids Res. 13:3101-3109; Van Heeke and Schuster, 1989, J. Biol. Chem. 264:5503-5509); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the  
15 presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned protective sequence product can be released from the GST moiety.

In an insect system, *Autographa californica*, nuclear polyhydrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda*  
20 cells. The protective sequence product coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of protective sequence product coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (*i.e.*,  
25 virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed. (*e.g.*, see Smith, *et al.*, 1983, J. Virol. 46:584; Smith, U.S. Patent No. 4,215,051).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the protective  
30 sequence product coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, *e.g.*, the late promoter and tripartite leader

sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (*e.g.*, region E1 or E3) will result in a recombinant virus that is viable and capable of expressing protective sequence products in infected hosts. (*See, e.g.*, Logan and Shenk, 1984, *Proc. Natl. Acad. Sci. USA* 81:3655-3659). Specific initiation signals may also be required for efficient translation of inserted protective sequence product coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where an entire protective sequence, including its own initiation codon and adjacent sequences, is inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only a portion of the protective sequence coding sequence is inserted, exogenous translational control signals, including, perhaps, the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, *etc.* (*see* Bittner, *et al.*, 1987, *Methods in Enzymol.* 153:516-544).

In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (*e.g.*, glycosylation) and processing (*e.g.*, cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells that possess the cellular machinery for proper processing of the primary transcript, glycosylation and phosphorylation of the gene product may be used. Such mammalian host cells include, but are not limited to, CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3 and WI38. Additional host cells derived from neuronal tissue include, but are not limited to, PC-12 cells and primary dissociated neurons which are removed from the brain and grown in culture.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines that stably express the protective sequence product may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (*e.g.*, promoter, enhancer, sequences, transcription terminators, polyadenylation sites, *etc.*), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines that express the protective sequence product. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that affect the endogenous activity of the protective sequence product.

A number of selection systems may be used, including, but not limited to, the herpes simplex virus thymidine kinase (Wigler, *et al.*, 1977, *Cell* 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska and Szybalski, 1962, *Proc. Natl. Acad. Sci. USA* 48:2026), and adenine phosphoribosyltransferase (Lowy, *et al.*, 1980, *Cell* 22:817) genes can be employed in *tk<sup>-</sup>*, *hgp<sup>r</sup>* or *ap<sup>r</sup>* cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: *dhfr*, which confers resistance to methotrexate (Wigler, *et al.*, 1980, *Proc. Natl. Acad. Sci. USA* 77:3567; O'Hare, *et al.*, 1981, *Proc. Natl. Acad. Sci. USA* 78:1527); *gpt*, which confers resistance to mycophenolic acid (Mulligan and Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072); *neo*, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, *et al.*, 1981, *J. Mol. Biol.* 150:1); and *hygro*, which confers resistance to hygromycin (Santerre, *et al.*, 1984, *Gene* 30:147).

Alternatively, the expression characteristics of an endogenous protective sequence within a cell line or microorganism may be modified by inserting a heterologous DNA regulatory element into the genome of a stable cell line or cloned microorganism such that the inserted regulatory element is operatively linked with the endogenous protective sequence. For example, an endogenous protective sequence which is normally "transcriptionally silent", *i.e.*, a protective sequence which is normally not expressed, or is



expressed only at very low levels in a cell line or microorganism, may be activated by inserting a regulatory element which is capable of promoting the expression of a normally expressed protective sequence product in that cell line or microorganism. Alternatively, a transcriptionally silent, endogenous protective sequence may be activated by insertion of a promiscuous regulatory element which works across cell types.

Methods, which are well known to those skilled in the art, can be used to construct vectors containing the protective sequence operatively associated with appropriate transcriptional/translational control signals. These methods include *in vitro* recombinant DNA techniques, and synthetic techniques. See, for example, the techniques described in Sambrook, *et al.*, 1992, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y. and Ausubel *et al.*, 1989, Current Protocols in Molecular Biology, Greene Publishing Associates & Wiley Interscience, N.Y.

The protective sequences may be associated operatively with a variety of different promoter/enhancer elements. The expression elements of these vectors may vary in their strength and specificities. Depending on the host/vector system utilized, any one of a number of suitable transcription and translation elements may be used. The promoter may be in the form of the promoter that is associated naturally with the gene of interest.

Alternatively, the DNA may be positioned under the control of a recombinant or heterologous promoter, *i.e.*, a promoter that is not associated normally with that gene. For example, tissue specific promoter/enhancer elements may be used to regulate the expression of the transferred DNA in specific cell types. Examples of transcriptional control regions which exhibit tissue specificity which have been described and could be used, include, but are not limited to:

choline acetyltransferase (ChAT) gene control region which is active in cholinergic cells in the brain (Lonnerberg *et al.*, 1996, JBC 271:33358-65; Lonnerberg *et al.*, 1995, PNAS 92: 4046-50; Ibenez and Perrson, 1991 Eur. J. Neurosci. 3: 1309-15), mouse Thy-1.2 gene control region which is active in adult neurons including hippocampus, thalamus, cerebellum, cortex, RGC, DRG, and MN in the brain (Caroni, 1997, J Neurosci. Meth. 71: 3-9; Vidal *et al.*, 1990, EMBO J 9: 833-40), neuron specific enolase (NSE) gene control region which is active in pan-neuronal, neuron specific, deep layers of cerebral and neocortex (not in white matter) areas of the brain (Hannas-Djebbara *et al.*, 1997, Brain Res. Mol. Brain Res. 46: 91-9; Peel *et al.*, 1997, Gene Therapy 4: 16-24; Twyman *et al.*, 1997, J Mol Neurosci 8: 63-73;

Forss-Petter *et al.*, 1990, Neuron 5:187-97), elastase I gene control region which is active in pancreatic acinar cells (Swift *et al.*, 1984, Cell 38:639-646; Ornitz *et al.*, 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:42S-51S); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122); immunoglobulin gene control region which is active in lymphoid cells (Grosschedl *et al.*, 1984, Cell 38:647-658; Adams *et al.*, 1985, Nature 318:533-538; Alexander *et al.*, 1987, Mol. Cell. Biol. 7:1436-1444); albumin gene control region which is active in liver (Pinkert *et al.*, 1987, Genes and Devel. 1:268-276); alpha-fetoprotein gene control region which is active in liver (Krumlauf *et al.*, 1985, Mol. Cell. Biol. 5:1639-1648; Hammer *et al.*, 1987, Science 235:53-58); alpha-1-antitrypsin gene control region which is active in liver (Kelsey *et al.*, 1987, Genes and Devel. 1:161-171); beta-globin gene control region which is active in myeloid cells (Magram *et al.*, 1985, Nature 315:338-340; Kollias *et al.*, 1986, Cell 46:89-94); myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead *et al.*, 1987, Cell 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Shani, 1985, Nature 314:283-286) and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason *et al.*, 1986, Science 234:1372-1378). Promoters isolated from the genome of viruses which grow in mammalian cells (*e.g.*, CMV, RSV, vaccinia virus 7.5K, SV40, HSV, adenoviruses MLP, and MMTV LTR promoters) may be used, as well as promoters produced by recombinant DNA or synthetic techniques. Further, promoters specifically activated within bone, *i.e.*, the osteocalcin promoter, which is specifically activated within cells of osteoblastic lineage, may be used to target expression of nucleic acids within bone cells.

A heterologous regulatory element may be inserted into a stable cell line or cloned microorganism, such that it is operatively linked with an endogenous protective sequence, using techniques, such as targeted homologous recombination, which are well known to those of skill in the art, and described *e.g.*, in Chappel, U.S. Patent No. 5,272,071; PCT publication No. WO 91/06667, published May 16, 1991.

Alternatively, utilizing an antibody specific for the fusion protein being expressed may readily purify any fusion protein. For example, a system described by Janknecht, *et al.* allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht, *et al.*, 1991, Proc. Natl. Acad. Sci. USA 88:8972-8976). In

this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the gene's open reading frame is translationally fused to an amino-terminal tag consisting of six histidine residues. Extracts from cells infected with recombinant vaccinia virus are loaded onto  $\text{Ni}^{2+}$ -nitriloacetic acid-agarose columns and histidine-tagged proteins are  
5 selectively eluted with imidazole-containing buffers.

The protective sequence products can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, sheep, cows and non-human primates, *e.g.*, baboons, monkeys and chimpanzees may be used to generate transgenic animals. The term "transgenic," as used  
10 herein, refers to animals expressing protective sequences from a different species (*e.g.*, mice expressing human protective sequences), as well as animals which have been genetically engineered to overexpress endogenous (*i.e.*, same species) sequences or animals which have been genetically engineered to no longer express endogenous protective sequences (*i.e.*, "knock-out" animals), and their progeny.

Any technique known in the art may be used to introduce a protective  
15 sequence transgene into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to, pronuclear microinjection (Hoppe and Wagner, 1989, U.S. Pat. No. 4,873,191); retrovirus mediated gene transfer into germ lines (Van der Putten, *et al.*, 1985, *Proc. Natl. Acad. Sci., USA* 82:6148-6152); gene targeting in embryonic  
20 stem cells (Thompson, *et al.*, 1989, *Cell* 56:313-321); electroporation of embryos (Lo, 1983, *Mol. Cell. Biol.* 3:1803-1814); and sperm-mediated gene transfer (Lavitrano *et al.*, 1989, *Cell* 57:717-723) (For a review of such techniques, see Gordon, 1989, *Transgenic Animals*, Intl. Rev. Cytol. 115, 171-229).

Any technique known in the art may be used to produce transgenic animal  
25 clones containing a protective sequence transgene, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal or adult cells induced to quiescence (Campbell, *et al.*, 1996, *Nature* 380:64-66; Wilmut, *et al.*, *Nature* 385:S10-S13).

The present invention provides for transgenic animals which carry a protective sequence transgene in all their cells, as well as animals which carry the transgene in some, but  
30 not all their cells, *i.e.*, mosaic animals. The transgene may be integrated as a single transgene or in concatamers, *e.g.*, head-to-head tandems or head-to-tail tandems. The transgene also

may be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko *et al.* (Lasko, *et al.*, 1992, *Proc. Natl. Acad. Sci. USA* 89:6232-6236). The regulatory sequences required for such a cell-type specific activation will depend on the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the cerebral transgene be integrated into the chromosomal site of the endogenous protective sequence, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleic acids homologous to the endogenous protective sequence are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleic acid of the endogenous protective sequence. The transgene also may be selectively introduced into a particular cell type, thus inactivating the endogenous protective sequence in only that cell type, by following, for example, the teaching of Gu, *et al.* (Gu, *et al.*, 1994, *Science* 265, 103-106). The regulatory sequences required for such a cell-type specific inactivation will depend on the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant protective sequence may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to assay whether integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include, but are not limited to, Northern blot analysis of tissue samples obtained from the animal, *in situ* hybridization analysis and RT-PCR (reverse transcriptase PCR). Samples of protective sequence-expressing tissue also may be evaluated immunocytochemically using antibodies specific for the transgene product.

Protective proteins can be used, *e.g.*, to treat cell death-related conditions, disorders, or diseases. Such protective sequence products include, but are not limited to, soluble derivatives such as peptides or polypeptides corresponding to one or more domains of the protective sequence product which are modified such that they are deleted for one or more hydrophobic domains. Alternatively, antibodies to the protein or anti-idiotypic antibodies which mimic the protective sequence product (including Fab fragments), modulators, antagonists or agonists can be used to treat cell death-related conditions, disorders, or

diseases involving the protective sequence product. In yet another approach, nucleotide constructs encoding such protective sequence products can be used to genetically engineer host cells to express such protective sequence products *in vivo*; these genetically engineered cells can function as "bioreactors" in the body delivering a continuous supply of protective sequence product, peptides and soluble polypeptides.

### 5.3 Antibodies to the Protective Sequence Products

Described herein are methods for the production of antibodies capable of specifically recognizing one or more protective sequence product epitopes or epitopes of conserved variants or peptide fragments of the protective sequence products of the invention. Further, antibodies that specifically recognize mutant forms of the protective sequence products of the invention are encompassed by the invention. The terms "specifically bind" and "specifically recognize" refer to antibodies which bind to protective sequence product epitopes involved in conditions, disorders, or diseases involving cell death at a higher affinity than they bind to protective sequence product epitopes not involved in such conditions, disorders, or diseases (*e.g.*, random epitopes).

Such antibodies may include, but are not limited to, polyclonal antibodies, monoclonal antibodies (mAbs), human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab')<sub>2</sub> fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies and epitope-binding fragments of any of the above. Such antibodies may be used, for example, in the detection of a protective sequence product in a biological sample and may, therefore, be utilized as part of a diagnostic or prognostic technique whereby patients may be tested for abnormal levels of protective sequence products, and/or for the presence of abnormal forms of such protective sequence products. Such antibodies also may be utilized in conjunction with, for example, compound screening schemes, as described, below, in Section 5.4.2, for the evaluation of the effect of test compounds on protective sequence product levels and/or activity. Additionally, such antibodies can be used in conjunction with the gene therapy techniques described below, in Section 5.4.1.3., to evaluate, for example, the normal and/or engineered cells prior to their introduction into the patient.

Antibodies derived from the protective sequence or protective sequence product, including, but not limited to, antibodies and anti-idiotypic antibodies that mimic activity or function additionally may be used in methods for inhibiting abnormal protective sequence product activity. Thus, such antibodies may, therefore, be utilized as part of treatment methods for protective sequence product-mediated conditions, disorders, or diseases.

For the production of antibodies against a protective sequence, various host animals may be immunized with a protective sequence or protective sequence product, or a portion thereof. Such host animals may include, but are not limited to, rabbits, mice and rats, to name but a few. Various adjuvants may be used to increase the immunological response, depending on the host species, including, but not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*.

Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen, such as protective sequence product, or an antigenic functional derivative thereof. For the production of polyclonal antibodies, host animals such as those described above, may be immunized with protective sequence product supplemented with adjuvants as also described above.

Monoclonal antibodies, which are homogeneous populations of antibodies to a particular antigen, may be obtained by any technique that provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique of Kohler and Milstein, (1975, *Nature* 256:495-497; and U.S. Patent No. 4,376,110), the human B-cell hybridoma technique (Kosbor *et al.*, 1983, *Immunology Today* 4:72; Cole *et al.*, 1983, *Proc. Natl. Acad. Sci. USA* 80:2026-2030), and the EBV-hybridoma technique (Cole *et al.*, 1985, *Monoclonal Antibodies And Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. The hybridoma producing the mAb of this invention may be cultivated *in vitro* or *in vivo*. Production of high titers of mAbs *in vivo* makes this the presently preferred method of production.

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, *e.g.*, Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarily determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, *e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better et al. (1988) *Science* 240:1041-1043; Liu et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu et al. (1987) *J. Immunol.* 139:3521-3526; Sun et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura et al. (1987) *Canc. Res.* 47:999-1005; Wood et al. (1985) *Nature* 314:446-449; and Shaw et al. (1988) *J. Natl. Cancer Inst.* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi et al. (1986) *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones et al. (1986) *Nature* 321:552-525; Verhoeyan et al. (1988) *Science* 239:1534; and Beidler et al. (1988) *J. Immunol.* 141:4053-4060.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Such antibodies can be produced, for example, using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, *e.g.*, all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently

undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995, *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Fremont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al. (1994) *Bio/technology* 12:899-903).

In addition, techniques developed for the production of "chimeric antibodies" (Morrison, et al., 1984, *Proc. Natl. Acad. Sci.*, 81:6851-6855; Neuberger, et al., 1984, *Nature* 312:604-608; Takeda, et al., 1985, *Nature*, 314:452-454) by splicing the genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, e.g., Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.)

In addition, techniques have been developed for the production of humanized antibodies. (See, e.g., Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) An immunoglobulin light or heavy chain variable region consists of a "framework" region interrupted by three hypervariable regions, referred to as complementarily determining regions (CDRs). The extent of the framework region and CDRs have been precisely defined (see, "Sequences of Proteins of Immunological Interest", Kabat, E. et al., U.S. Department of Health and Human Services (1983) ). Briefly, humanized antibodies are antibody molecules from non-human species having one or more



CDRs from the non-human species and a framework region from a human immunoglobulin molecule.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778; Bird, 1988, *Science* 242:423-426; Huston, *et al.*, 1988, *Proc. Natl. Acad. Sci. USA* 85:5879-5883; and Ward, *et al.*, 1989, *Nature* 334:544-546) can be adapted to produce single chain antibodies against protective sequence products. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide.

Antibody fragments that recognize specific epitopes may be generated by known techniques. For example, such fragments include, but are not limited to: the F(ab')<sub>2</sub> fragments, which can be produced by pepsin digestion of the antibody molecule and the Fab fragments, which can be generated by reducing the disulfide bridges of the F(ab')<sub>2</sub> fragments. Alternatively, Fab expression libraries may be constructed (Huse, *et al.*, 1989, *Science* 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

#### 5.4 Uses of the Protective Sequences. Protective Sequence Products and Antibodies

Described herein are various uses and applications of protective sequences, protective sequence products, including peptide fragments and fusion proteins thereof and of antibodies and anti-idiotypic antibodies derived from the protective sequence products and peptide fragments thereof. The application relates to compositions and methods for the treatment of conditions, disorders, or diseases involving cell death. Such applications include, but are not limited to, the prophylactic or therapeutic use of protective sequences which, when introduced into a cell predisposed to undergo cell death or in the process of dying, to prevent, delay, or rescue a cell, cells, tissue, organs, or organisms from dying, as described below in Section 5.4.1

Additionally, such applications include methods for the treatment of conditions, disorders, or diseases involving cell death, including, but not limited to, those associated with the central nervous system including neurological and psychiatric conditions, disorders, or diseases, and others as described below, in Section 5.4.1.1, and for the

identification of compounds which modulate the expression of the protective sequence and/or the synthesis or activity of the protective sequence product, as described below, in Section 5.4.1. Such compounds can include, for example, other cellular products that are involved in such processes as the regulation of cell death. These compounds can be used, for example, in the amelioration of conditions, disorders, or diseases involving cell death.

One example of the type of injury that can cause cell death in neuronal cells is stroke, which often is the result of ischemic injury. A relatively broad time window (8 hours to perhaps several days or longer) exists between the onset of ischemic injury (*i.e.* cessation or marked reduction in blood flow) before most neural cells actually die. There are many complex pathways and perhaps hundreds of different signaling molecules which are likely to be involved, leaving many different intervention points each with the potential to prevent, delay, arrest and reverse the cell death program. These delayed biochemical intervention points represent ideal clinical intervention points as they correspond to the time period during which most stroke patients present for medical treatment.

Many current medications for the treatment of stroke affect the physical and biochemical events that are acutely related to the initial onset of stroke, and, thus, must be administered soon after the biochemical cascades begin. These approaches all suffer from the necessity of administering the drugs within a very brief time window following a stroke. However, many stroke patients do not even realize that they have suffered from a stroke until a time point at which many of the current treatments are ineffective. This is because many stroke patients often do not present at the emergency room prior to the passing of at least 13 hours from the onset of the stroke. The methods and compounds of the present invention, however, can be administered during the broader time window between stroke and the onset of the pathways leading to cell death.

In addition to stroke, a variety of other conditions, disorders, and diseases lead to the activation of the same biochemical cascades which lead to neuronal cell death in stroke. There is growing evidence that numerous other disease states that induce cell death programs are related to those induced by stroke. Cell death programs have been increasingly implicated in Alzheimer's disease, a well-known neurodegenerative condition which leads to substantial loss of specific neuronal populations in the neocortex and hippocampus. Vascular dementia (multi-infarct dementia) is another disorder in which stroke-like cell death pathways

are active. In vascular dementia, a repetitive process of small blood vessel diseases induces regional brain cell death, leading to a progressive loss of cognitive abilities. A partial list of other brain diseases which activate brain cell death pathways similar to those observed in stroke include, but are not limited to, Parkinson's disease, traumatic injury, Down's syndrome, Huntington's disease, HIV infection and intracranial infections.

One notable example from the preceding list is physical trauma to the nervous system. Although such trauma can be caused by a multitude of different physical insults to the head, neck, spine and other parts of the nervous system, all result in focal damage to, and death of, neural tissue and its component cells. Focally damaged areas behave similarly to stroke-induced infarcts in that a wider area of neural damage and death, a penumbra, is induced via biochemical and cellular mechanisms which are similar or identical to those occurring in stroke.

While, for clarity, the uses described in this section are primarily uses related to conditions, disorders, or diseases involving cell death, it is to be noted that each of the diagnostic and therapeutic treatments described herein can be additionally utilized in connection with other defects associated with the protective sequences of the invention.

Additionally, described herein are various applications of protective sequences, protective sequence products, genes, gene products, and/or their regulatory elements, including, but not limited to, prognostic and diagnostic evaluation of conditions, disorders, or diseases as described below in Section 5.4.1.1.

A variety of methods can be employed for the diagnostic and prognostic evaluation of conditions, disorders, or diseases involving cell death and for the identification of subjects having a predisposition to such conditions, disorders, or diseases.

Since protective sequences or protective sequence products need not normally be involved in all conditions, disorders, or diseases involving cell death, methods of the invention include, for example, modulating the expression of the protective sequence and/or the activity of the protective sequence product for the treatment of conditions, disorders, or diseases involving cell death which are normally mediated by some other gene.

For cell death related conditions, disorders, or diseases in which the protective sequences or protective sequence products are involved normally, such diagnostic and prognostic methods may, for example, utilize reagents such as the protective nucleic acids

described in Section 5.1, and antibodies directed against protective sequence products, including peptide fragments thereof, as described, above, in Section 5.3.

Specifically, such reagents may be used, for example, for:

- (1) the detection of the presence of protective sequence mutations, or the  
5 detection of either over- or under-expression of the protective sequence relative to wild-type levels of expression;
- (2) the detection of over- or under-abundance of protective sequence products relative to wild-type abundance of the protective sequence product; and
- (3) the detection of an aberrant level of protective sequence product activity  
10 relative to wild-type protective sequence product activity levels.

Protective nucleic acids can, for example, be used to diagnose a condition, disorder, or disease involving cell death using, for example, the techniques for mutation/polymorphism detection described above in Section 5.1.

- 15 Mutations at a number of different genetic loci may lead to phenotypes related to conditions, disorders, or diseases involving cell death. Ideally, the treatment of patients suffering from such conditions, disorders, or diseases will be designed to target the particular genetic loci containing the mutation mediating the condition, disorder, or disease. Genetic polymorphisms have been linked to differences in drug effectiveness. Thus, identification of alterations in protective sequence, protein or gene flanking regions can be utilized in  
20 pharmacogenetic methods to optimize therapeutic drug treatments.

- In one embodiment of the present invention, therefore, alterations, *i.e.*, polymorphisms, in the protective sequence or protein encoded by genes comprising such polymorphisms, are associated with a drug or drugs' efficacy, tolerance or toxicity, and may be used in pharmacogenomic methods to optimize therapeutic drug treatments, including  
25 therapeutic drug treatments for one of the conditions, disorders, or diseases described herein contained in Section 5.4.1.1, *e.g.*, central nervous system conditions, disorders, or diseases. Such polymorphisms can be used, for example, to refine the design of drugs by decreasing the incidence of adverse events in drug tolerance studies, *e.g.*, by identifying patient subpopulations of individuals who respond or do not respond to a particular drug therapy in  
30 efficacy studies, wherein the subpopulations have a polymorphism associated with drug responsiveness or unresponsiveness. The pharmacogenomic methods of the present invention

also can provide tools to identify new drug targets for designing drugs and to optimize the use of already existing drugs, *e.g.*, to increase the response rate to a drug and/or to identify and exclude non-responders from certain drug treatments (*e.g.*, individuals having a particular polymorphism associated with unresponsiveness or inferior responsiveness to the drug treatment) or to decrease the undesirable side effects of certain drug treatments and/or to identify and exclude individuals with marked susceptibility to such side effects (*e.g.*, individuals having a particular polymorphism associated with an undesirable side effect to the drug treatment).

In an embodiment of the present invention, polymorphisms in the protective sequence or flanking this sequence, or variations in protective sequence expression, or activity, *e.g.*, variations due to altered methylation, differential splicing or post-translational modification of the protective sequence product, may be utilized to identify an individual having a disease or condition resulting from a disorder involving cell death and thus define the most effective and safest drug treatment. Assays such as those described herein may be used to identify such polymorphisms or variations in protective sequence expression or activity. Once a polymorphism in the protective sequence or in a flanking sequence in linkage disequilibrium with a disorder-causing allele, or a variation in protective sequence expression has been identified in an individual, an appropriate drug treatment can be prescribed to the individual.

For the detection of protective sequence mutations or polymorphisms, any nucleated cell can be used as a starting source for genomic nucleic acid. For the detection of protective sequence expression or protective sequence products, any cell type or tissue in which the protective sequence is expressed may be utilized.

Nucleic acid-based detection techniques are described, below, in Section 5.4.1.4. Peptide detection techniques are described, below, in Section 5.4.1.5.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits. The invention therefore also encompasses kits for detecting the presence of a polypeptide or nucleic acid of the invention in a biological sample (*i.e.*, a test sample). Such kits can be used, *e.g.*, to determine if a subject is suffering from or is at increased risk of developing a condition, disorder, or disease associated with a disorder-causing allele, or aberrant expression or activity of a polypeptide of the invention. For

example, the kit can comprise a labeled compound or agent capable of detecting the polypeptide or mRNA or DNA or protective sequence sequences, *e.g.*, encoding the polypeptide in a biological sample. The kit can comprise further a means for determining the amount of the polypeptide or mRNA in the sample (*e.g.*, an antibody that binds the polypeptide or an oligonucleotide probe that binds to DNA or mRNA encoding the polypeptide). Kits can also include instructions for observing that the tested subject is suffering from, or is at risk of developing, a condition, disorder, or disease associated with aberrant expression of the polypeptide if the amount of the polypeptide or mRNA encoding the polypeptide is above or below a normal level, or if the DNA correlates with presence of an allele which causes a condition, disorder, or disease.

For antibody-based kits, the kit can comprise, for example: (1) a first antibody (*e.g.*, attached to a solid support) which binds to a polypeptide of the invention; and, optionally, (2) a second, different antibody which binds to either the polypeptide or to the first antibody and is conjugated to a detectable agent.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide (*e.g.*, a detectably labeled oligonucleotide) which hybridizes to a nucleic acid sequence encoding a polypeptide of the invention, or (2) a pair of primers useful for amplifying a nucleic acid molecule encoding a polypeptide of the invention.

The kit also can comprise, for example, one or more buffering agents, preservatives or protein stabilizing agents. The kit also can comprise components necessary for detecting the detectable agent (*e.g.*, an enzyme or a substrate). The kit can contain also a control sample or a series of control samples that can be assayed and compared to the test sample. Each component of the kit usually is enclosed within an individual container and all of the various containers are within a single package along with instructions for observing whether the tested subject is suffering from or is at risk of developing a condition, disorder, or disease associated with polymorphisms which correlate with alleles which cause conditions, disorders, or diseases involving cell death, and/or aberrant levels of mRNA, polypeptides or activity.

Additionally, the application relates to the compositions and methods for the development of screening assays for the identification of compounds, described in Section

5.4.2 below, which interact with or modulate protective sequences, protective sequence products, genes, gene products, and/or their regulatory elements.

#### 5.4.1 Composition and Methods for the Treatment of Conditions, Disorders, or Diseases Involving Cell Death

This application relates to compositions and methods for the treatment of conditions, disorders, or diseases involving cell death. Such applications include, but are not limited to, the prophylactic or therapeutic use of protective sequences, protective sequence products, genes, gene products, or the regulatory elements, target sequences, or variants of any of the aforementioned sequences or products, which, when introduced into a cell predisposed to undergo cell death or in the process of dying, prevent, delay, or rescue a cell, cells, tissue, organs, or organisms from dying. The application further relates to the methods and compositions whereby a condition, disorder, or disease involving cell death, including but not limited to, the conditions, disorders, or diseases mentioned in Section 5.4.1.1, may be treated wherein such methods can comprise administering antibodies, antisense molecules or sequences, ribozyme molecules, or other inhibitors or modulators directed against such protective sequences, protective sequence products, genes, gene products, or the regulatory elements, target sequences, or variants of any of the aforementioned sequences or products.

The application relates to compositions and methods for those instances whereby the condition, disorder, or disease involving cell death results from protective sequence mutations, such methods can comprise supplying the subject with a nucleic acid molecule encoding an unimpaired protective sequence product such that an unimpaired protective sequence product is expressed and the cell, cells, tissue, organ, organism displaying symptoms of the condition, disorder, or disease is prevented, delayed, or rescued from death.

In another embodiment of methods for the treatment of conditions, disorders, or diseases involving cell death resulting from protective sequence mutations, such methods can comprise supplying the subject with a cell comprising a nucleic acid molecule which encodes an unimpaired protective sequence product such that the cell expresses the unimpaired protective sequence product and the cell, cells, tissue, organ, or organism displaying symptoms of the condition, disorder, or disease is prevented, delayed, or rescued

from death.

In cases in which a loss of normal protective sequence product function results in the development of a condition, disorder, or disease involving cell death, an increase in protective sequence product activity would facilitate progress towards an asymptomatic state in individuals exhibiting a deficient level of protective sequence expression and/or gene product activity. Methods for enhancing the expression or synthesis of protective sequence product can include, for example, methods such as those described below, in Section 5.4.1.3.

Alternatively, symptoms of a condition, disorder, or disease involving cell death may be prevented, delayed, or rescued by administering a compound which decreases the level of protective sequence expression and/or gene product activity. Methods for inhibiting or reducing the level of protective sequence product synthesis or expression can include, for example, methods such as those described in Section 5.4.1.2.

In cases where the development of a condition, disorder, or disease involving cell death is due to a sequence or gene other than a protective sequence, modulating, including but not limited to, mimicking, agonizing, or antagonizing the expression of a protective sequence and/or the activity of a protective sequence product, or their regulatory elements, can be used for the treatment of the condition, disorder, or disease involving cell death. This is because protective sequences are nucleic acid molecules comprising nucleic acid sequences which, when introduced into a cell predisposed to undergo cell death, prevent, delay, or rescue such cell death relative to a corresponding cell into which no exogenous protective sequence has been introduced.

The proteins and peptides which may be used in the methods of the invention include synthetic (*e.g.*, recombinant or chemically synthesized) proteins and peptides, as well as naturally occurring proteins and peptides. The proteins and peptides may have both naturally occurring and non-naturally occurring amino acid residues (*e.g.*, D-amino acid residues) and/or one or more non-peptide bonds (*e.g.*, imino, ester, hydrazide, semicarbazide, and azo bonds). The proteins or peptides may also contain additional chemical groups (*i.e.*, functional groups) present at the amino and/or carboxy termini, such that, for example, the stability, bioavailability, and/or inhibitory activity of the peptide is enhanced. Exemplary functional groups include hydrophobic groups (*e.g.* carbobenzoxy, dansyl, and t-butyloxycarbonyl, groups), an acetyl group, a 9-fluorenylmethoxy-carbonyl group and



macromolecular carrier groups (*e.g.*, lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates) including peptide groups. Additional proteins and peptides which may be used in the methods of the invention include those described in WO 99/59615, which is herein incorporated by reference in its entirety.

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#### **5.4.1.1 Examples of Conditions, Disorders, or Diseases Involving Cell Death**

The types of conditions, disorders, or diseases which can be prevented, delayed, or rescued by the compounds and methods of the present invention include, but are not limited to, those associated with the central nervous system including neurological and psychiatric conditions, disorders, or diseases; those of the peripheral nervous system; conditions, disorders, or diseases caused by physical injury; conditions, disorders, or diseases of the blood vessels or heart; conditions, disorders, or diseases of the respiratory system; neoplastic conditions, disorders, or diseases; conditions, disorders, or diseases of blood cells; conditions, disorders, or diseases of the gastrointestinal tract; conditions, disorders, or diseases of the liver; conditions, disorders, or diseases of the pancreas; conditions, disorders, or diseases of the kidney; conditions, disorders, or diseases of the ureters, urethra or bladder; conditions, disorders, or diseases of the male genital system; conditions, disorders, or diseases of the female genital tract; conditions, disorders, or diseases of the breast; conditions, disorders, or diseases of the endocrine system; conditions, disorders, or diseases of the thymus or pineal gland; conditions, disorders, or diseases of the skin or mucosa; conditions, disorders, or diseases of the musculoskeletal system; conditions, disorders, or diseases causing a fluid or hemodynamic derangement; inherited conditions, disorders, or diseases; conditions, disorders, or diseases of the immune system or spleen; conditions, disorders, or diseases caused by a nutritional disease; and conditions, disorders, or diseases typically occurring in infancy or childhood.

Conditions, disorders, or diseases involving the central nervous system include, but are not limited to, common pathophysiologic complications such as increased intracranial pressure and cerebral herniation, septic embolism, cerebral edema, suppurative endovascularitis and hydrocephalus; infections such as meningitis, acute meningitis, acute lymphocytic meningitis, chronic meningitis, purulent meningitis, syphilitic gumma,

encephalitis, cerebral abscess, epidural abscess, subdural abscess, brain abscess, viral encephalitis, acute viral encephalitis, encephal meningitis, aseptic meningitis, post-infectious encephalitis, subacute encephalitis, chronic encephalitis, chronic meningitis, chronic encephal meningitis, slow virus diseases and unconventional agent encephalopathies;

5 protozoal infections such as malaria, toxoplasmosis, amebiasis and trypanosomiasis; rickettsial infections such as typhus and Rocky Mountain spotted fever; metazoal infections such as echinococcosis and cysticercosis; vascular diseases such as ischemic encephalopathy, cerebral infarction, intracranial hemorrhage, intraparenchymal hemorrhage, subarachnoid hemorrhage, mixed intraparenchymal and subarachnoid hemorrhage; conditions involving the

10 eye such as macular degeneration, glaucoma, retinopathy of prematurity, retinitis pigmentosa, diabetic retinopathy, or other traumatic injuries to the retina or optic nerve; trauma such as epidural hematoma, subdural hematoma, parenchymal injuries; tumors such as primary intracranial tumors, astrocytoma, oligodendroglioma, ependymoma, medulloblastoma and meningioma; degenerative diseases such as Alzheimer's disease, Huntington's disease,

15 Parkinsonism, idiopathic Parkinson's disease and motor neuron disease; demyelinating diseases such as multiple sclerosis; nutritional, environmental and metabolic conditions, disorders, or diseases.

Conditions, disorders, or diseases of the peripheral nervous system include, but are not limited to, peripheral neuropathy, acute idiopathic polyneuropathy, diabetic

20 neuropathy and peripheral nerve tumors.

Conditions, disorders, or diseases caused by physical injury include, but are not limited to, the direct, indirect, immediate, or delayed effects of: changes in temperature such as frostbite and thermal burns; an increase in atmospheric pressure such as air blast or immersion blast caused by an explosion; a decrease in atmospheric pressure such as caisson

25 disease or high-altitude hypoxia; mechanical violence from penetrating or non-penetrating traumatic injury; electromechanical energy such as radiation injury from either charged particles or electromagnetic waves; electrocution or non-ionizing radiation such as radio waves, microwaves, laser light or ultrasound.

Conditions, disorders, or diseases of the blood vessels or heart include, but are not limited to, hypertension (high blood pressure), heart failure; ischemic or atherosclerotic heart disease; myocardial infarction; cardiac arrest; hypertensive heart disease; cor

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pulmonale; valvular heart disease such as that caused by rheumatic fever, aortic valve stenosis, mitral annulus calcification, carcinoid heart disease, nonbacterial thrombotic endocarditis, or nonbacterial verrucous endocarditis; infectious endocarditis caused by organisms including, but not limited to, Streptococcus species, Staphylococcus species, enterococci, pneumococci, gram-negative rods, Candida species, Aspergillus species, or culture-negative endocarditis; congenital heart disease such as atrial septal defect, ventricular septal defect, patent ductus arteriosus, coarctation of the aorta, Tetralogy of Fallot, tricuspid atresia, pulmonary stenosis or atresia, aortic stenosis or atresia, bicuspid aortic valve, or hypoplastic left heart syndrome; cardiomyopathy; pericarditis; pericardial effusion; rheumatoid heart disease; congenital anomalies of the blood vessels; arteriosclerosis including, but not limited to atherosclerosis, Monckeberg's medial calcific stenosis, hyaline arteriosclerosis, or hyperplastic arteriosclerosis; one or more of the vasculidities including, but not limited to, polyarteritis nodosa, hypersensitivity angiitis, Wegener's granulomatosis, giant cell (temporal) arteritis, Takayasu's arteritis, Kawasaki's disease, thromboangiitis obliterans, infectious vasculitis, Raynaud's disease; arteriosclerotic aortic aneurysm; syphilitic aortic aneurysm; dissecting aortic aneurysm; varicose veins; thrombophlebitis; lymphangitis; lymphedema; telangiectases; or arteriovenous malformations (AVM).

Conditions, disorders, or diseases of the respiratory system include, but are not limited to, pulmonary congestion; heart failure; embolism; infarction; pulmonary hypertension; adult respiratory distress syndrome (ARDS); obstructive lung disease; restrictive lung disease; chronic obstructive pulmonary disease; asthma; sarcoidosis; diffuse interstitial or infiltrative lung diseases including, but not limited to, idiopathic pulmonary fibrosis, pneumoconiosis, hypersensitivity pneumonitis, Goodpasture's syndrome, idiopathic pulmonary hemosiderosis, collagen-vascular diseases, or pulmonary eosinophilia; serofibrinous pleuritis; suppurative pleuritis; hemorrhagic pleuritis; pleural effusions; pneumothorax; hemothorax or pneumohemothorax.

Neoplastic conditions, disorders, or diseases include, but are not limited to, benign tumors composed of one parenchymal cell type such as fibromas, myxomas, lipomas, hemangiomas, meningiomas, leiomyomas, adenomas, nevi, moles, or papillomas; benign mixed tumors derived from one germ layer such as a mixed tumor of salivary gland origin; benign mixed tumors derived from more than one germ layer such as a teratoma; primary

malignant tumors or metastases of malignant tumors composed of one parenchymal cell type  
 such as sarcomas, Ewing's tumor, leukemia, myeloma, histiocytosis X, Hodgkin's disease,  
 lymphomas, carcinomas, melanomas, bronchial adenoma, small cell lung cancer, or  
 seminoma; primary malignant tumors or metastases of mixed malignant tumors derived from  
 5 one germ layer such as Wilms' tumor or malignant mixed salivary gland tumor; primary  
 malignant tumor or metastases of mixed malignant tumors derived from one germ layer such  
 as malignant teratoma or teratocarcinoma; undifferentiated benign tumor or undifferentiated  
 malignant tumor.

Conditions, disorders, or diseases of blood cells include, but are not limited to,  
 10 anemia due to one or more of the following conditions: acute blood loss, chronic blood loss,  
 hemolytic anemia, sickle cell disease, thalassemia syndromes, autoimmune hemolytic anemia,  
 traumatic anemia, or diminished erythropoiesis from megaloblastic anemia, iron deficiency,  
 aplastic anemia, idiopathic bone marrow failure; polycythemia; hemorrhagic diatheses related  
 to increased vascular fragility; hemorrhagic diatheses related to a reduction in platelets;  
 15 idiopathic or thrombotic thrombocytopenic purpura; hemorrhagic diatheses related to  
 defective platelet function; hemorrhagic diatheses related to abnormalities in clotting  
 factor(s); disseminated intravascular coagulation (DIC); neutropenia; agranulocytosis;  
 leukocytosis; plasma cell dyscrasias such as myeloma, Waldenstrom's macroglobulinemia, or  
 heavy-chain disease; or histiocytosis.

20 Conditions, disorders, or diseases of the gastrointestinal tract include, but are  
 not limited to, congenital anomalies such as atresia, fistulas, or stenosis; periodontal disease;  
 periapical disease; xerostomia; necrotizing sialometaplasia; esophageal rings or webs; hernia;  
 Mallory-Weiss syndrome; esophagitis; diverticulosis; diverticulitis; scleroderma; esophageal  
 varices; acute or chronic gastritis; peptic ulcer; gastric erosion or ulceration; ischemic bowel  
 25 disease; infarction; embolism; Crohn's disease; obstruction from foreign bodies, hernia,  
 adhesion, intussusception, or volvulus; ileus; megacolon; angiodysplasia; ulcerative colitis;  
 pseudomembranous colitis; or polyps.

Conditions, disorders, or diseases of the liver include, but are not limited to,  
 acute hepatic failure due to one of more of metabolic, circulatory, toxic, microbial, or  
 30 neoplastic causes; chronic hepatic failure due to one or more of metabolic, circulatory, toxic,  
 microbial, or neoplastic causes; hereditary hyperbilirubinemias; infarct; embolism; hepatic

circulation thrombosis or obstruction; fulminant hepatic necrosis; portal hypertension; alcoholic liver disease; post-necrotic cirrhosis; biliary cirrhosis; cirrhosis associated with alpha-1-antitrypsin deficiency; Wilson's disease; or Reye's syndrome.

5 Conditions, disorders, or diseases of the pancreas include, but are not limited to, congenital aberrant pancreas, congenital anomalies of pancreatic ducts, stromal fatty infiltration, pancreatic atrophy, acute hemorrhagic pancreatitis, chronic pancreatitis, chronic calcifying pancreatitis, chronic obstructive pancreatitis, pancreatic pseudocyst, diabetes mellitus, or gestational diabetes.

10 Conditions, disorders, or diseases of the kidney include, but are not limited to, congenital anomalies; polycystic renal disease; dialysis-associated cystic disease; glomerular disease, including, but not limited to, acute glomerulonephritis, acute proliferative glomerulonephritis, rapidly progressive glomerulonephritis, postinfectious rapidly progressive glomerulonephritis, Goodpasture's syndrome, idiopathic rapidly progressive glomerulonephritis, nephrotic syndrome, membranous glomerulonephritis, lipoid nephrosis, 15 focal segmental glomerulosclerosis, membranoproliferative glomerulonephritis, focal proliferative glomerulonephritis, chronic glomerulonephritis, or hereditary nephritis; acute tubular necrosis; acute renal failure; tubulointerstitial diseases including, but not limited to, pyelonephritis, drug-induced interstitial nephritis, analgesic nephritis, urate nephropathy, hypercalcemia and nephrocalcinosis, hypokalemic nephropathy, myeloma-induced 20 tubulointerstitial disease, radiation nephritis, immunologically mediated tubulointerstitial disease; hypertension; malignant hypertension; renal artery stenosis; renal diseases secondary to microangiopathic hemolytic anemia; atheroembolic renal disease; sickle cell disease nephropathy; diffuse cortical necrosis; renal infarcts; obstructive uropathy; or urolithiasis.

25 Conditions, disorders, or diseases of the ureters, urethra or bladder include, but are not limited to, congenital anomalies; inflammatory diseases; physical obstruction by causes including, but not limited to calculi, strictures, neoplasia, blood clot, or pregnancy; sclerosing retroperitonitis; acute cystitis; chronic cystitis; interstitial cystitis; emphysematous cystitis; eosinophilic cystitis; encrusted cystitis; fistula; or neurogenic bladder.

30 Conditions, disorders, or diseases of the male genital system include, but are not limited to, congenital anomalies; balanoposthitis; condyloma; phimosis; paraphimosis; dysplastic epithelial lesions; nonspecific epididymitis or orchitis; granulomatous orchitis;

torsion of the testis or its vascular supply; granulomatous prostatitis; acute or chronic prostatitis; or benign prostatic hyperplasia.

Conditions, disorders, or diseases of the female genital tract include, but are not limited to, congenital anomalies, lichen scleroses, acute cervicitis, chronic cervicitis, cervical polyps; acute endometritis; chronic endometritis; endometriosis; dysfunctional uterine bleeding; endometrial hyperplasia; senile cystic endometrial atrophy; salpingitis; polycystic ovary disease; pre-eclampsia or eclampsia (toxemia of pregnancy); placentitis; threatened abortion; or ectopic pregnancy.

Conditions, disorders, or diseases of the breast include, but are not limited to, congenital anomalies, acute mastitis, chronic mastitis, galactoceles, granulomas, traumatic fat necrosis, mammary duct ectasia, fibrocystic disease, sclerosing adenitis, epithelial hyperplasia, hypertrophy, or gynecomastia.

Conditions, disorders, or diseases of the endocrine system include, but are not limited to, congenital anomalies; Sheehan's pituitary necrosis; empty sella syndrome; hyperthyroidism (thyrotoxicosis) from causes including, but not limited to, Graves' disease, toxic multinodular goiter, toxic adenoma, acute or subacute thyroiditis, TSH-secreting tumor, neonatal thyrotoxicosis, iatrogenic thyrotoxicosis; Hashimoto's thyroiditis; hypothyroidism (cretinism or myxedema) from causes including, but not limited to, surgical or radioactive ablation, primary idiopathic myxedema, iodine deficiency, goitrogenic agents, hypopituitarism, hypothalamic lesions, TSH resistance, subacute thyroiditis, or chronic thyroiditis; diffuse nontoxic simple or multinodular goiter; multiple endocrine neoplasia syndromes; primary or secondary hyperparathyroidism; chief cell hyperplasia; clear cell hyperplasia; hypoparathyroidism; pseudo- and pseudopseudohypoparathyroidism; Addison's disease; Waterhouse-Friderichsen syndrome; secondary adrenocortical insufficiency; Cushing's syndrome; Conn's syndrome; or congenital adrenal hyperplasia.

Conditions, disorders, or diseases of the skin or mucosa include, but are not limited to, melanocytic proliferative disorders; inflammatory dermatoses including, but not limited to, eczematous dermatitis, urticaria, erythema multiforme, cutaneous necrotizing vasculitis, cutaneous lupus erythematosus, graft-versus-host disease, panniculitis, acne vulgaris, rosacea, lichen planus, lichen sclerosus et atrophicus, pityriasis, psoriasis, or parapsoriasis; blistering diseases including, but not limited to, pemphigus, bullous

pemphigoid, dermatitis herpetiformis, or porphyria.

Conditions, disorders, or diseases of the musculoskeletal system include, but are not limited to, muscular atrophy; segmental necrosis; myositis; muscular dystrophy, including, but not limited to, Duchenne type, Becker type, Fascioscapulohumeral, Limb-  
 5 Girdle, myotonic dystrophy, or ocular myopathy; congenital myopathies; myasthenia gravis; traumatic myositis ossificans; nodular fasciitis; desmoid tumors; palmar fibromatosis; congenital bone disorders including, but not limited to, osteogenesis imperfecta, achondroplasia, osteopetrosis, osteochondromatosis, endochondromatosis; osteomyelitis; fractures; osteoporosis; osteomalacia; bony changes secondary to hyperparathyroidism;  
 10 Paget's disease; hypertrophic osteoarthropathy; fibrous dysplasia; or nonossifying fibroma.

Conditions, disorders, or diseases causing a fluid or hemodynamic derangement include, but are not limited to, systemic edema; anasarca; edema from increased hydrostatic pressure including, but not limited to congestive heart failure, cirrhosis of the liver, constrictive pericarditis, venous obstruction; edema from reduced oncotic pressure  
 15 including, but not limited to, cirrhosis of the liver, malnutrition, protein-losing renal disease, protein-losing gastroenteropathy, protein loss through increased vascular permeability; edema from lymphatic obstruction including, but not limited to, cancer, inflammatory injury, surgical injury, traumatic injury, or radiation injury; edema from increased osmotic tension in the interstitial fluid including, but not limited to, sodium retention from excessive salt intake  
 20 or increased renal sodium retention, reduced renal perfusion, acute or chronic renal failure, acute or chronic renal insufficiency; edema from increased endothelial permeability including, but not limited to, inflammation, shock, burns, trauma, allergic reaction, immunologic reaction, or adult respiratory distress syndrome; ascites; pericardial effusion; hydrothorax; hyperemia; hemorrhage; mural thrombus or occlusive thrombus diminishing or  
 25 obstructing vascular flow; phlebothrombosis; blood clot; embolism; thromboembolism; disseminated intravascular coagulation (DIC); amniotic fluid infusion; amniotic fluid embolism; systemic embolism disease; septic embolism; fat embolism; pulmonary embolism; air gas embolism (caisson disease or decompression sickness); anemic (white) infarction; hemorrhagic (red) infarction; cerebral infarction; septic infarction; ischemia; cardiogenic  
 30 shock from conditions including, but not limited to, myocardial infarction, cardiac arrest, cardiac rupture, cardiac tamponade, pulmonary embolism, cardiac valvular obstruction, or

cardiac arrhythmias; hypovolemic shock from conditions including, but not limited to, hemorrhage, vomiting, diarrhea, diaphoresis, extensive injury to bone or soft tissues, burns, or accumulation of intraperitoneal fluid; shock due to peripheral blood pooling from conditions including, but not limited to, spinal cord injury, general anesthesia, regional anesthesia, local  
5 anesthesia, drug-induced ganglionic or adrenergic blockade, gram-negative septicemia, or gram-positive septicemia; anaphylaxis, or disseminated intravascular coagulation (DIC).

Inherited conditions, disorders, or diseases include, but are not limited to, Down's syndrome, Edwards' syndrome, Patau's syndrome, other trisomies, Cri du Chat syndrome, Klinefelter's syndrome, XYY syndrome, Turner's syndrome, Multi-X female  
10 syndrome, hermaphroditism or pseudohermaphroditism, Marfan's syndrome, neurofibromatosis, vonHippel-Lindau disease, familial hypercholesterolemia, albinism, alkaptonuria, Fabry's disease, Fragile-X syndrome, Ehlers-Danlos syndromes, inherited neoplastic syndromes, inherited autosomal dominant conditions, Huntington's disease, Alport's disease, sickle-cell disease, thalassemia, tuberous sclerosis, vonWillebrand's disease, polycystic kidney disease,  
15 Pompe's disease, GM1-gangliosidosis; Tay-Sachs disease, Sandhoff-Jatzkewitz disease, metachromatic leukodystrophy, multiple sulfatase deficiency, Krabbe's disease, Gaucher's disease, Niemann-Pick disease, all types of mucopolysaccharidoses, I-cell disease, Hurler's polydystrophy, fucosidosis, mannosidosis, aspartylglycosaminuria, Wolman's disease, or acid phosphatase deficiency, inherited autosomal recessive conditions, inherited sex-linked  
20 conditions.

Conditions, disorders, or diseases of the immune system or spleen include, but are not limited to, Type I hypersensitivity conditions (anaphylaxis and other basophil or mast cell mediated conditions), Type II hypersensitivity conditions (cytotoxic conditions involving phagocytosis or lysis of target cell), Type III hypersensitivity conditions (immune complex  
25 conditions involving antigen-antibody complexes), Type IV hypersensitivity conditions (cell-mediated conditions), transplant rejection, systemic lupus erythematosus, Sjogren's syndrome, CREST, scleroderma, polymyositis-dermatomyositis, mixed connective tissue disease, polyarteritis nodosa, amyloidosis, X-linked agammaglobulinemia, common variable immunodeficiency, isolated IgA deficiency, DiGeorge's syndrome, severe combined  
30 immunodeficiency, Wiscott-Aldrich syndrome, infection with HIV virus, acquired immune deficiency syndrome (AIDS), congenital anomalies of the immune system, hypersplenism,



splenomegaly, congenital anomalies of the spleen, congestive splenomegaly, infarcts, or splenic rupture.

Conditions, disorders, or diseases caused by a nutritional disease include, but are not limited to, marasmus, kwashiorkor, fat-soluble vitamin deficiency or toxicity (Vitamins A, D, E, or K), water-soluble vitamin deficiency or toxicity (thiamine, riboflavin, niacin, pyridoxine, folate, cobalamin, Vitamin C), mineral deficiency or toxicity (iron, calcium, magnesium, sodium, potassium, chloride, zinc, copper, iodine, cobalt, chromium, selenium, nickel, vanadium, manganese, molybdenum, rickets, osteomalacia, beriberi, hypoprothrombinemia, pellagra, megaloblastic anemia, scurvy, pernicious anemia, lack of gastric intrinsic factor, removal or pathophysiological functioning in the terminal ileum, microcytic anemia, or obesity.

Conditions, disorders, or diseases typically occurring in infancy or childhood include, but are not limited to, preterm birth, congenital malformations from genetic causes, congenital malformations from infectious causes, congenital malformations from toxic or teratogenic causes, congenital malformations from radiation, congenital malformations from idiopathic causes, small for gestational age infants, perinatal trauma, perinatal asphyxia, perinatal ischemia or hypoxia, birth injury, intracranial hemorrhage, deformations, respiratory distress syndrome of the newborn, atelectasis, hemolytic disease of the newborn, kernicterus, hydrops fetalis, congenital anemia of the newborn, icterus gravis, phenylketonuria, galactosemia, cystic fibrosis, hamartoma, or choristoma.

In another embodiment, the compounds and methods of the invention can be used to treat infections that cause cell death. The infections may be caused by bacteria; viruses; members of the family rickettsiae or chlamydia; fungi, yeast, hyphae or pseudohyphae; prions; protozoas; or metazoas.

Examples of aerobic or anaerobic bacteria which may cause such infections include, but are not limited to, gram-positive cocci, gram-positive bacilli (gram-positive rods), gram-negative cocci, gram-negative bacilli (gram-negative rods), Mycoplasma species, Ureaplasma species, Treponema species, Leptospira species, Borrelia species, Vibrio species, Mycobacteria species, members of Actinomycetes or L-forms (cell-wall deficient forms).

Examples of DNA, RNA or both DNA and RNA viruses which may cause such infections include, but are not limited to, members of the families adenoviridae,

parvoviridae, papovaviridae, herpesviridae, poxviridae, picornaviridae, orthomyxoviridae, paramyxoviridae, rhabdoviridae, bunyaviridae, arenaviridae, coronaviridae, retroviridae, reoviridae, togaviridae and caliciviridae.

5 Examples of members of the families rickettsiae or chlamydiae which may cause such infections include, but are not limited to, Rickettsia species, Rochalimaea species, Coxiella species or Chlamydia species.

10 Examples of fungi, yeast, hyphae or pseudohyphae which may cause such infections include, but are not limited to, members of Ascomycota, Basidiomycota, Zygomycota, or Deuteromycota (Fungi Imperfecti); Candida species, Cryptococcus species, Torulopsis species, Rhodotorula species, Sporothrix species, Phialophora species, Cladosporium species, Xylomyces species, Blastomyces species, Histoplasma species, Coccidioides species, Paracoccidioides species, Geotrichum species, Aspergillus species, Rhizopus species, Mucor species, Pseudoallescheria species or Absidia species.

15 Examples of prions which may cause such infections include, but are not limited to, the causative agent of Creutzfeldt-Jakob Disease, the causative agent of Gerstmann-Straussler-Scheinker Disease, the causative agent of fatal familial insomnia, the causative agent of kuru, and the causative agent of bovine spongiform encephalopathy.

20 Examples of protozoa at any point in their life cycle which may cause such infections include, but are not limited to, Entamoeba species, Naegleria species, Acanthamoeba species, Pneumocystis species, Balantidium species, members of order Leptomyxida, Plasmodium species, Toxoplasma species, Leishmania species and Trypanosoma species.

25 Examples of metazoa at any point in their life cycle which may cause such infections include, but are not limited to, members of Platyhelminthes such as the organisms in Cestoda (tapeworms) or Trematoda (flukes); or members of Aschelminthes such as the organisms in Acanthocephala, Chaetognatha, Cyclophora, Gastrotricha, Nematoda or Rotifera.

30 In a further embodiment, the compounds and methods of the invention can be used to treat infections or disorders which cause cell death in organ systems including, but not limited to, blood vessels, heart, red blood cells, white blood cells, lymph nodes, spleen, respiratory system, oral cavity, gastrointestinal tract, liver and biliary tract, pancreas, kidney.

lower urinary tract, upper urinary tract and bladder, male sexual organs and genitalia, female sexual organs and genitalia, breast, thyroid gland, adrenal gland, parathyroid gland, skin, musculoskeletal system, bone marrow or bones.

In a further embodiment, the compounds and methods of the invention can be used to treat further physiological impacts on organs caused by the infections which induce cell death including, but not limited to, fever equal to or greater than 101.5 degrees Fahrenheit, a decrease or increase in pulse rate by more than 20 beats per minute, a decrease or increase in supine systolic blood pressure by more than 30 millimeters of mercury, an increase or decrease in respiratory rate by more than 8 breaths per minute, an increase or decrease in blood pH by more than 0.10 pH units, an increase or decrease in one or more serum electrolytes outside of the clinical laboratory's usual reference range, an increase or decrease in the partial pressure of arterial oxygen or carbon dioxide outside of the clinical laboratory's usual reference range, an increase or decrease in white or red blood cells outside of the laboratory's usual reference range, an acute confusional state such as delirium where delirium is defined by the American Psychiatric Association's DSM-IV Manual or a diminished level of consciousness or attention.

#### **5.4.1.2 Modulatory Antisense, Ribozyme and Triple Helix Approaches**

In another embodiment, the types of conditions, disorders, or diseases involving cell death which may be prevented, delayed, or rescued by modulating protective sequence expression, protective sequence product activity, or their regulatory elements by using protective sequences in conjunction with well-known antisense, gene "knock-out," ribozyme and/or triple helix methods, are described. Among the compounds which may exhibit the ability to modulate the activity, expression or synthesis of the protective sequence, the protective sequence product, or its regulatory elements, including the ability to prevent, delay, or rescue a cell, cells, tissue, organ, or organism from the symptoms of a condition, disorder, or disease involving cell death are antisense, ribozyme and triple helix molecules. Such molecules may be designed to modulate, reduce or inhibit either unimpaired, or if appropriate, mutant protective sequence activity. Techniques for the production and use of such molecules are well known to those of skill in the art.

Antisense RNA and DNA molecules act to directly block the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense approaches involve the design of oligonucleotides which are complementary to a protective sequence mRNA. The antisense oligonucleotides will bind to the complementary protective sequence mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required.

A sequence "complementary" to a portion of an RNA, as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

In one embodiment, oligonucleotides complementary to non-coding regions of the protective sequence of interest could be used in an antisense approach to inhibit translation of endogenous mRNA. Antisense nucleic acids should be at least six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects, the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

Regardless of the choice of target sequence, it is preferred that *in vitro* studies are first performed to quantitate the ability of the antisense oligonucleotide to inhibit protective sequence expression. It is preferred that these studies utilize controls that distinguish between antisense gene inhibition and nonspecific biological effects of oligonucleotides. It is also preferred that these studies compare levels of the cerebral RNA or protein with that of an internal control RNA or protein. Additionally, it is envisioned that results obtained using the antisense oligonucleotide are compared with those obtained using a control oligonucleotide. It is preferred that the control oligonucleotide is of approximately the same length as the test oligonucleotide and that the nucleic acid of the oligonucleotide

differs from the antisense sequence no more than is necessary to prevent specific hybridization to the target sequence.

The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger, *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre, *et al.*, 1987, *Proc. Natl. Acad. Sci. U.S.A.* 84:648-652; PCT Publication No. WO88/09810, published December 15, 1988) or the blood-brain barrier (see, *e.g.*, PCT Publication No. WO89/10134, published April 25, 1988), hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

5 In yet another embodiment, the antisense oligonucleotide is an a-anomeric oligonucleotide. An a-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual b-units, the strands run parallel to each other (Gautier, *et al.*, 1987, *Nucl. Acids Res.* 15:6625-6641). The oligonucleotide is a 2'-O-methylribonucleotide (Inoue, *et al.*, 1987, *Nucl. Acids Res.* 15:6131-6148), or a chimeric  
10 RNA-DNA analogue (Inoue, *et al.*, 1987, *FEBS Lett.* 215:327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, *e.g.*, by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein, *et al.* (1988, *Nucl. Acids Res.*  
15 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin, *et al.*, 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:7448-7451), *etc.*

While antisense nucleotides complementary to the protective sequence coding region sequence could be used, those complementary to the transcribed, untranslated region are most preferred.

20 Antisense molecules should be delivered to cells that express the protective sequence *in vivo*. A number of methods have been developed for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies which specifically bind receptors or antigens expressed on the target  
25 cell surface) can be administered systemically.

A preferred approach to achieve intracellular concentrations of the antisense sufficient to suppress translation of endogenous mRNAs utilizes a recombinant DNA construct in which the antisense oligonucleotide is placed under the control of a strong pol III or pol II promoter. The use of such a construct to transfect target cells in the patient will  
30 result in the transcription of sufficient amounts of single stranded RNAs which will form complementary base pairs with the endogenous protective sequence transcripts and thereby

prevent translation of the protective sequence mRNA. For example, a vector can be introduced *e.g.*, such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in mammalian, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, *Nature* 290:304-310), the promoter contained in the 3'-long terminal repeat of Rous sarcoma virus (Yamamoto, *et al.*, 1980, *Cell* 22:787-797), the herpes thymidine kinase promoter (Wagner, *et al.*, 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster, *et al.*, 1982, *Nature* 296:39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used that selectively infect the desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically).

Ribozyme molecules designed to catalytically cleave target gene mRNA transcripts can also be used to prevent translation of target gene mRNA and, therefore, expression of target gene product. (See, *e.g.*, PCT International Publication WO90/11364, published October 4, 1990; Sarver, *et al.*, 1990, *Science* 247, 1222-1225).

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. (For a review, see Rossi, 1994, *Current Biology* 4:469-471). The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage event. The composition of ribozyme molecules must include one or more sequences complementary to the target gene mRNA, and must include the well known catalytic sequence responsible for mRNA cleavage. For this sequence, see, *e.g.*, U.S. Patent No. 5,093,246, which is incorporated herein by reference in its entirety.

While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy target gene mRNAs, the use of hammerhead ribozymes is preferred.

Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions which form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Myers, 5 1995, *Molecular Biology and Biotechnology: A Comprehensive Desk Reference*, VCH Publishers, New York, (see especially Figure 4, page 833) and in Haseloff and Gerlach, 1988, *Nature*, 334:585-591, which is incorporated herein by reference in its entirety.

Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the target gene mRNA, *i.e.*, to increase efficiency and minimize the 10 intracellular accumulation of non-functional mRNA transcripts.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one which occurs naturally in *Tetrahymena thermophila* (known as the IVS, or L-19 IVS RNA) and which has been extensively described by Thomas Cech and collaborators (Zaug, *et al.*, 1984, *Science*, 224:574-578; Zaug and Cech, 15 1986, *Science*, 231:470-475; Zaug, *et al.*, 1986, *Nature*, 324:429-433; published International patent application No. WO 88/04300 by University Patents Inc.; Been and Cech, 1986, *Cell*, 47:207-216). The Cech-type ribozymes have an eight base pair active site that hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes that target eight base-pair active site sequences that 20 are present in the target gene.

As in the antisense approach, the ribozymes can be composed of modified oligonucleotides (*e.g.*, for improved stability, targeting, *etc.*) and should be delivered to cells that express the target gene *in vivo*. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II 25 promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous target gene messages and inhibit translation. Because ribozymes, unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Endogenous target gene expression can also be reduced by inactivating or 30 "knocking out" the target gene or its promoter using targeted homologous recombination (*e.g.*, see Smithies, *et al.*, 1985, *Nature* 317:230-234; Thomas and Capecchi, 1987, *Cell*



51:503-512; Thompson, *et al.*, 1989, *Cell* 5:313-321; each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional target gene (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous target gene (either the coding regions or regulatory regions of the target gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells which express the target gene *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the target gene. Such approaches are particularly suited in the agricultural field where modifications to ES (embryonic stem) cells can be used to generate animal offspring with an inactive target gene (*e.g.*, see Thomas and Capecchi, 1987 and Thompson, 1989, *supra*). However this approach can be adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors.

Alternatively, endogenous target gene expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the target gene (*i.e.*, the target gene promoter and/or enhancers) to form triple helical structures which prevent transcription of the target gene in target cells in the body. (See generally, Helene, 1991, *Anticancer Drug Des.*, 6(6):569-584; Helene, *et al.*, 1992, *Ann. N.Y. Acad. Sci.*, 660:27-36; and Maher, 1992, *Bioassays* 14(12):807-815).

Nucleic acid molecules to be used in triple helix formation for the inhibition of transcription should be single stranded and composed of deoxynucleotides. The base composition of these oligonucleotides must be designed to promote triple helix formation via Hoogsteen base pairing rules, which generally require sizable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleic acids may be pyrimidine-based, which will result in TAT and CGC<sup>+</sup> triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen which are purine-rich, for example, contain a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in GGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so-called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizable stretch of either purines or pyrimidines to be present on one strand of a duplex.

In instances wherein the antisense, ribozyme, and/or triple helix molecules described herein are utilized to inhibit mutant gene expression, it is possible that the technique may so efficiently reduce or inhibit the transcription (triple helix) and/or translation (antisense, ribozyme) of mRNA produced by normal target gene alleles which the possibility may arise wherein the concentration of normal target gene product present may be lower than is necessary for a normal phenotype. In such cases, to ensure that substantially normal levels of target gene activity are maintained, therefore, nucleic acid molecules which encode and express target gene polypeptides exhibiting normal target gene activity may be introduced into cells via gene therapy methods such as those described, below, in Section 5.4.1.3 which do not contain sequences susceptible to whatever antisense, ribozyme, or triple helix treatments are being utilized. Alternatively, in instances whereby the target gene encodes an extracellular protein, it may be preferable to co-administer normal target gene protein in order to maintain the requisite level of target gene activity.

Anti-sense RNA and DNA, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules, as discussed above. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid-phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors that incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

### 5.4.1.3 Gene Replacement Therapy

Protective nucleic acid sequences, described above in Section 5.1, can be utilized for transferring recombinant protective nucleic acid sequences to cells and expressing said sequences in recipient cells. Such techniques can be used, for example, in marking cells or for the treatment of a condition, disorder, or disease involving cell death. Such treatment can be in the form of gene replacement therapy. Specifically, one or more copies of a normal protective sequence or a portion of the protective sequence which directs the production of a protective sequence product exhibiting normal protective sequence function, may be inserted into the appropriate cells within a patient, using vectors which include, but are not limited to adenovirus, adeno-associated virus and retrovirus vectors, in addition to other particles which introduce DNA into cells, such as liposomes.

Because the protective sequence of the invention may be expressed in the brain, such gene replacement therapy techniques should be capable of delivering protective sequences to these cell types within patients. Thus, in one embodiment, techniques which are well known to those of skill in the art (see, *e.g.*, PCT Publication No. WO89/10134, published April 25, 1988) can be used to enable protective sequences to cross the blood-brain barrier readily and to deliver the sequences to cells in the brain. With respect to delivery which is capable of crossing the blood-brain barrier, viral vectors such as, for example, those described above, are preferable.

In another embodiment, techniques for delivery involve direct administration, *e.g.*, by stereotactic delivery of such protective sequences to the site of the cells in which the protective sequences are to be expressed.

Methods for introducing genes for expression in mammalian cells are well known in the field. Generally, for such gene therapy methods, the nucleic acid is directly administered *in vivo* into a target cell or a transgenic mouse that expresses SP-10 promoter operably linked to a reporter gene. This can be accomplished by any methods known in the art, *e.g.*, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, *e.g.*, by infection using a defective or attenuated retroviral or other viral vector (see U.S. Patent No. 4,980,286), by direct injection of naked DNA, by use of microparticle bombardment (*e.g.*, a gene gun; Biolistic, Dupont), by coating with lipids or cell-surface receptors or transfecting agents, by encapsulation in

liposomes, microparticles, or microcapsules, by administering it in linkage to a peptide which is known to enter the nucleus, or by administering it in linkage to a ligand subject to receptor-mediated endocytosis (see e.g., Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432), which can be used to target cell types specifically expressing the receptors. In another embodiment, a nucleic acid-ligand complex can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted *in vivo* for cell specific uptake and expression, by targeting a specific receptor (see, e.g., PCT Publications WO 92/06180 dated April 16, 1992; WO 92/22635 dated December 23, 1992; WO92/20316 dated November 26, 1992; WO93/14188 dated July 22, 1993; WO 93/20221 dated October 14, 1993).

Additional methods which may be utilized to increase the overall level of protective sequence expression and/or gene product activity include using targeted homologous recombination methods, discussed in Section 5.2, above, to modify the expression characteristics of an endogenous protective sequence in a cell or microorganism by inserting a heterologous DNA regulatory element such that the inserted regulatory element is operatively linked with the endogenous protective sequence in question. Targeted homologous recombination can thus be used to activate transcription of an endogenous protective sequence which is "transcriptionally silent", *i.e.*, is not normally expressed or is normally expressed at very low levels, or to enhance the expression of an endogenous protective sequence which is normally expressed.

Further, the overall level of protective sequence expression and/or gene product activity may be increased by the introduction of appropriate protective sequence-expressing cells, preferably autologous cells, into a patient at positions and in numbers which are sufficient to ameliorate the symptoms of a condition, disorder, or disease involving cell death. Such cells may be either recombinant or non-recombinant.

Among the cells that can be administered to increase the overall level of protective sequence expression in a patient are normal cells, preferably brain cells, which express the protective sequence. Alternatively, cells, preferably autologous cells, can be engineered to express protective sequences, and may then be introduced into a patient in positions appropriate for the amelioration of the symptoms of a condition, disorder, or disease involving cell death. Alternately, cells which express an unimpaired protective sequence and

which are from a MHC matched individual can be utilized, and may include, for example, brain cells. The expression of the protective sequences is controlled by the appropriate gene regulatory sequences to allow such expression in the necessary cell types. Such gene regulatory sequences are well known to the skilled artisan. Such cell-based gene therapy techniques are well known to those skilled in the art, see, *e.g.*, Anderson, U.S. Patent No. 5,399,349.

When the cells to be administered are non-autologous cells, they can be administered using well-known techniques that prevent a host immune response against the introduced cells from developing. For example, the cells may be introduced in an encapsulated form that, while allowing for an exchange of components with the immediate extracellular environment, does not allow the introduced cells to be recognized by the host immune system.

Additionally, compounds, such as those identified via techniques such as those described, in Section 5.4.2, which are capable of modulating protective sequences, protective sequence product activity, or their regulatory sequences can be administered using standard techniques which are well known to those of skill in the art. In instances in which the compounds to be administered are to involve an interaction with brain cells, the administration techniques should include well known methods that allow for a crossing of the blood-brain barrier.

#### **5.4.1.4 Detection of Protective Nucleic Acid Molecules**

A variety of methods can be employed to screen for the presence of protective sequence-specific mutations or polymorphisms (including polymorphisms flanking protective sequences) and to detect and/or assay levels of protective nucleic acid sequences.

Mutations or polymorphisms within or flanking the protective sequences can be detected by utilizing a number of techniques. Nucleic acid from any nucleated cell can be used as the starting point for such assay techniques, and may be isolated according to standard nucleic acid preparation procedures that are well known to those of skill in the art.

Protective nucleic acid sequences may be used in hybridization or amplification assays of biological samples to detect abnormalities involving protective sequence structure, including point mutations, insertions, deletions, inversions, translocations

and chromosomal rearrangements. Such assays may include, but are not limited to, Southern analyses, single-stranded conformational polymorphism analyses (SSCP) and PCR analyses.

Diagnostic methods for the detection of protective sequence-specific mutations or polymorphisms can involve for example, contacting and incubating nucleic acids obtained from a sample, *e.g.*, derived from a patient sample or other appropriate cellular source with one or more labeled nucleic acid reagents including recombinant DNA molecules, cloned genes or degenerate variants thereof, such as described in Section 5.1, above, under conditions favorable for the specific annealing of these reagents to their complementary sequences within or flanking the protective sequence. The diagnostic methods of the present invention further encompass contacting and incubating nucleic acids for the detection of single nucleotide mutations or polymorphisms of the protective sequence. Preferably, these nucleic acid reagent sequences within the protective sequence are 15 to 30 nucleotides in length.

After incubation, all non-annealed nucleic acids are removed from the reaction. The presence of nucleic acids that have hybridized, if any such molecules exist, is then detected. Using such a detection scheme, the nucleic acid from the cell type or tissue of interest can be immobilized, for example, to a solid support such as a membrane, or a plastic surface such as that on a microtiter plate or polystyrene beads. In this case, after incubation, non-annealed, labeled nucleic acid reagents of the type described in Section 5.1 are easily removed. Detection of the remaining, annealed, labeled nucleic acid reagents is accomplished using standard techniques well known to those skilled in the art. The protective sequences of the invention to which the nucleic acid reagents have annealed can be compared to the annealing pattern expected from a normal protective sequence of the invention in order to determine whether a protective sequence mutation is present.

In a preferred embodiment, protective sequence mutations or polymorphisms can be detected by using a microassay of nucleic acid sequences of the invention immobilized to a substrate or "gene chip" (see, *e.g.* Cronin, et al., 1996, Human Mutation 7:244-255). Alternative diagnostic methods for the detection of protective sequence-specific nucleic acid molecules (or flanking sequences), in patient samples or other appropriate cell sources, may involve their amplification, *e.g.*, by PCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), followed by the analysis of the amplified molecules using

techniques well known to those of skill in the art, such as, for example, those listed above. The resulting amplified sequences can be compared to those which would be expected if the nucleic acid being amplified contained only normal copies of the protective sequence in order to determine whether a protective sequence mutation or polymorphism in linkage disequilibrium with a disease-causing allele exists.

Among those nucleic acid sequences that are preferred for such amplification-related diagnostic screening analyses are oligonucleotide primers that amplify exon sequences. The sequences of such oligonucleotide primers are, therefore, preferably derived from cerebral intron sequences so that the entire exon, or coding region, can be analyzed as discussed below. Primer pairs useful for amplification of cerebral exons are preferably derived from adjacent introns. Appropriate primer pairs can be chosen such that each of the cerebral exons present within the gene will be amplified. Primers for the amplification of exons can be routinely designed by one of ordinary skill.

Additional nucleic acid sequences which are preferred for such amplification-related analyses are those which will detect the presence of a polymorphism which differs from the sequence depicted in the Figures. Such polymorphisms include ones that represent mutations associated with a condition, disorder, or disease involving cell death.

Amplification techniques are well known to those of skill in the art and can routinely be utilized in connection with primers such as those described above. In general, hybridization conditions can be as follows: In general, for probes between 14 and 70 nucleotides in length, the melting temperature  $T_m$  is calculated using the formula:  $T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log[\text{monovalent cations}]) + 0.41(\% \text{ G+C}) - (500/N)$  where  $N$  is the length of the probe. If the hybridization is carried out in a solution containing formamide, the melting temperature is calculated using the equation  $T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log[\text{monovalent cations}]) + 0.41(\% \text{ G+C}) - (0.61\% \text{ formamide}) - (500/N)$  where  $N$  is the length of the probe. Additionally, well-known genotyping techniques can be performed to identify individuals carrying protective sequence mutations. Such techniques include, for example, the use of restriction fragment length polymorphisms (RFLPs), which involve sequence variations in one of the recognition sites for the specific restriction enzyme used.

Further, improved methods for analyzing DNA polymorphisms, which can be utilized for the identification of protective sequence-specific mutations, have been described

which capitalize on the presence of variable numbers of short, tandemly repeated DNA sequences between the restriction enzyme sites. For example, Weber (U.S. Pat. No. 5,075,217) describes a DNA marker based on length polymorphisms in blocks of (dC-dA)<sub>n</sub>-(dG-dT)<sub>n</sub> short tandem repeats. The average separation of (dC-dA)<sub>n</sub>-(dG-dT)<sub>n</sub> blocks is estimated to be 30,000-60,000 bp. Markers which are so closely spaced exhibit a high frequency of co-inheritance, and are extremely useful in the identification of genetic mutations, such as, for example, mutations within the protective sequence of the invention, and the diagnosis of diseases and disorders related to mutations of the protective sequences of the invention.

Also, Caskey *et al.* (U.S. Pat.No. 5,364,759) describe a DNA profiling assay for detecting short tri- and tetra nucleotide repeat sequences. The process includes extracting the DNA of interest, amplifying the extracted DNA and labeling the repeat sequences to form a genotypic map of the individual's DNA.

Other methods well known in the art may be used to identify single nucleotide polymorphisms (SNPs), including biallelic SNPs or biallelic markers which have two alleles, both of which are present at a fairly high frequency in a population. Conventional techniques for detecting SNPs include, *e.g.*, conventional dot blot analysis, single stranded conformational polymorphism (SSCP) analysis (see, *e.g.*, Orita *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:2766-2770), denaturing gradient gel electrophoresis (DGGE), heteroduplex analysis, mismatch cleavage detection and other routine techniques well known in the art (see, *e.g.*, Sheffield *et al.*, 1989, *Proc. Natl. Acad. Sci.* 86:5855-5892; Grompe, 1993, *Nature Genetics* 5:111-117). Alternative, preferred methods of detecting and mapping SNPs involve microsequencing techniques wherein an SNP site in a target DNA is detecting by a single nucleotide primer extension reaction (see, *e.g.*, Goelet *et al.*, PCT Publication No.

WO92/15712; Mundy, U.S. Patent No. 4,656,127; Vary and Diamond, U.S. Patent No. 4,851,331; Cohen *et al.*, PCT Publication No. WO91/02087; Chee *et al.*, PCT Publication No. WO95/11995; Landegren *et al.*, 1988, *Science* 241:1077-1080; Nicerson *et al.*, 1990, *Proc. Natl. Acad. Sci. U.S.A.* 87:8923-8927; Pastinen *et al.*, 1997, *Genome Res.* 7:606-614; Pastinen *et al.*, 1996, *Clin. Chem.* 42:1391-1397; Jalanko *et al.*, 1992, *Clin. Chem.* 38:39-43; Shumaker *et al.*, 1996, *Hum. Mutation* 7:346-354; Caskey *et al.*, PCT Publication No. WO 95/00669).



The level of protective sequence expression also can be assayed. For example, RNA from a cell type or tissue known, or suspected, to express the protective sequence, such as brain, may be isolated and tested utilizing hybridization or PCR techniques such as are described, above. The isolated cells can be derived from cell culture or from a patient. The analysis of cells taken from culture may be a necessary step in the assessment of cells to be used as part of a cell-based gene therapy technique or, alternatively, to test the effect of compounds on the expression of the protective sequence. Such analyses may reveal both quantitative and qualitative aspects of the expression pattern of the protective sequence, including activation or inactivation of protective sequence expression.

In one embodiment of such a detection scheme, a cDNA molecule is synthesized from an RNA molecule of interest (*e.g.*, by reverse transcription of the RNA molecule into cDNA). A sequence within the cDNA is then used as the template for a nucleic acid amplification reaction, such as a PCR amplification reaction, or the like. The nucleic acid reagents used as synthesis initiation reagents (*e.g.*, primers) in the reverse transcription and nucleic acid amplification steps of this method are chosen from among the protective sequence nucleic acid reagents described in Section 5.1. The preferred lengths of such nucleic acid reagents are at least 9-30 nucleotides. For detection of the amplified product, the nucleic acid amplification may be performed using radioactively or non-radioactively labeled nucleotides. Alternatively, enough amplified product may be made such that the product may be visualized by standard ethidium bromide staining or by utilizing any other suitable nucleic acid staining method.

Additionally, it is possible to perform such protective sequence expression assays "*in situ*", *i.e.*, directly upon tissue sections (fixed and/or frozen) of patient tissue obtained from biopsies or resections, such that no nucleic acid purification is necessary. Nucleic acid reagents such as those described in Section 5.1 may be used as probes and/or primers for such *in situ* procedures (see, for example, Nuovo, G.J., 1992, "PCR In Situ Hybridization: Protocols And Applications", Raven Press, NY).

Alternatively, if a sufficient quantity of the appropriate cells can be obtained, standard Northern blot analysis can be performed to determine the level of mRNA expression of the protective sequence.

#### 5.4.1.5 Detection of Protective Sequence Products

Protective sequence products of the invention, including both wild-type and mutant protective sequence products, conserved variants and polypeptide fragments thereof, which are discussed, above, in Section 5.2, may be detected using antibodies which are directed against such gene products. Such antibodies, which are discussed in Section 5.3, above, may thereby be used as diagnostics and prognostics for a condition, disorder, or disease involving cell death. Such methods may be used to detect abnormalities in the level of protective sequence expression or of protective sequence product synthesis, or abnormalities in the structure, temporal expression and/or physical location of protective sequence product. The antibodies and immunoassay methods described herein have, for example, important *in vitro* applications in assessing the efficacy of treatments for conditions, disorders, or diseases involving cell death. Antibodies, or fragments of antibodies, such as those described below, may be used to screen potentially therapeutic compounds *in vitro* to determine their effects on protective sequence expression and protective sequence product production. The compounds which have beneficial effects on conditions, disorders, or diseases involving cell death can thereby be identified, and a therapeutically effective dose determined.

*In vitro* immunoassays may also be used, for example, to assess the efficacy of cell-based gene therapy for a condition, disorder, or disease involving cell death. Antibodies directed against protective sequence products may be used *in vitro* to determine, for example, the level of protective sequence expression achieved in cells genetically engineered to produce the protective sequence product. In the case of intracellular protective sequence products, such an assessment is done, preferably, using cell lysates or extracts. Such analysis will allow for a determination of the number of transformed cells necessary to achieve therapeutic efficacy *in vivo*, as well as optimization of the gene replacement protocol.

The tissue or cell type to be analyzed generally will include those that are known, or suspected, to express the protective sequence. The protein isolation methods employed herein may, for example, be such as those described in Harlow and Lane (1988, "Antibodies: A Laboratory Manual", Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York). The isolated cells can be derived from cell culture or from a patient. The analysis of cells taken from culture may be a necessary step in the assessment of cells to

be used as part of a cell-based gene therapy technique or, alternatively, to test the effect of compounds on the expression of the protective sequence.

Preferred diagnostic methods for the detection of protective sequence products, conserved variants or peptide fragments thereof, may involve, for example, immunoassays wherein the protective sequence products or conserved variants or peptide fragments are detected by their interaction with an anti-protective sequence product-specific antibody.

For example, antibodies, or fragments of antibodies, such as those described, above, in Section 5.3, may be used to, quantitatively or qualitatively, detect the presence of protective sequence products or conserved variants or peptide fragments thereof. This can be accomplished, for example, by immunofluorescence techniques employing a fluorescently labeled antibody (see below, this Section) coupled with light microscopic, flow cytometric or fluorimetric detection. Such techniques are especially preferred for protective sequence products that are expressed on the cell surface.

The antibodies (or fragments thereof) useful in the present invention may, additionally, be employed histologically, as in immunofluorescence or immunoelectron microscopy, for *in situ* detection of protective sequence products, conserved variants or peptide fragments thereof. *In situ* detection may be accomplished by removing a histological specimen from a patient, and applying thereto a labeled antibody which binds to a protective sequence polypeptide. The antibody (or fragment) is preferably applied by overlaying the labeled antibody (or fragment) onto a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of the protective sequence product, conserved variants or peptide fragments, but also its distribution in the examined tissue. Using the present invention, those of ordinary skill will readily recognize that any of a wide variety of histological methods (such as staining procedures) can be modified in order to achieve *in situ* detection of a protective sequence product.

Immunoassays for protective sequence products, conserved variants or peptide fragments thereof will typically comprise incubating a sample, such as a biological fluid, a tissue extract, freshly harvested cells or lysates of cells in the presence of a detectably labeled antibody capable of identifying the protective sequence product, conserved variants or peptide

fragments thereof, and detecting the bound antibody by any of a number of techniques well-known in the art.

The biological sample may be brought in contact with and immobilized onto a solid phase support or carrier, such as nitrocellulose, which is capable of immobilizing cells, cell particles or soluble proteins. The support may then be washed with suitable buffers followed by treatment with the detectably labeled protective sequence product specific antibody. The solid phase support may then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support may then be detected by conventional means.

By "solid phase support or carrier" is intended any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads. Those skilled in the art will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

One of the ways in which the protective sequence product-specific antibody can be detectably labeled is by linking the same to an enzyme, such as for use in an enzyme immunoassay (EIA) (Voller, A., "The Enzyme Linked Immunosorbent Assay (ELISA)", 1978, Diagnostic Horizons 2:1-7, Microbiological Associates Quarterly Publication, Walkersville, MD); Voller, A. *et al.*, 1978, *J. Clin. Pathol.* 31:507-520; Butler, J.E., 1981, *Meth. Enzymol.* 73:482-523; Maggio, E. (ed.), 1980, Enzyme Immunoassay, CRC Press, Boca Raton, FL.; Ishikawa, E. *et al.*, (eds.), 1981, Enzyme Immunoassay, Kaku Shoin, Tokyo). The enzyme that is bound to the antibody will react with an appropriate substrate, preferably a chromogenic substrate, in such a manner as to produce a chemical moiety which can be detected, for example, by spectrophotometric, fluorimetric or by visual means.

Enzymes which can be used to detectably label the antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase,  $\alpha$ -glycerophosphate dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase,  
5 b-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase. The detection can be accomplished by colorimetric methods that employ a chromogenic substrate for the enzyme. Detection also may be accomplished by visual comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

10 Detection may be accomplished also using any of a variety of other immunoassays. For example, by radioactively labeling the antibodies or antibody fragments, it is possible to detect protective sequence products through the use of a radioimmunoassay (RIA) (*see*, for example, Weintraub, B., Principles of Radioimmunoassays, Seventh Training Course on Radioligand Assay Techniques, The Endocrine Society, March, 1986). The  
15 radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or by autoradiography.

It is also possible to label the antibody with a fluorescent compound. When the fluorescently labeled antibody is exposed to light of the proper wavelength, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent  
20 labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, *o*-phthaldehyde and fluorescamine.

The antibody can also be detectably labeled using fluorescence emitting metals such as  $^{152}\text{Eu}$ , or others of the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as diethylenetriaminepentaacetic acid (DTPA) or  
25 ethylenediaminetetraacetic acid (EDTA).

The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds  
30 are luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used to label the antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

#### 5.4.2 Screening Assays for Compounds which Interact with Protective Sequence Products or Modulate Protective Sequence Activity

The following assays are designed to identify compounds which bind to a protective sequence product, compounds which bind to proteins, or portions of proteins which interact with a protective sequence product, compounds which modulate, *e.g.*, interfere with, the interaction of a protective sequence product with proteins and compounds which modulate the activity of the protective sequence (*i.e.*, modulate the level of protective sequence expression and/or modulate the level of protective sequence product activity). Assays may additionally be utilized which identify compounds which bind to protective sequence regulatory sequences (*e.g.*, promoter sequences; see *e.g.*, Platt, 1994, J. Biol. Chem. 269, 28558-28562), and which can modulate the level of protective sequence expression. Such compounds may include, but are not limited to, small organic molecules, such as ones which are able to cross the blood-brain barrier, gain to and/or entry into an appropriate cell and affect expression of the protective sequence or some other gene involved in a protective sequence regulatory pathway.

Methods for the identification of such proteins are described, below, in Section 5.4.2.2. Such proteins may be involved in the control and/or regulation of functions related to cell death. Further, among these compounds are compounds which affect the level of protective sequence expression and/or protective sequence product activity and which can be used in the therapeutic treatment of conditions, disorders, or diseases involving cell death as described, below, in Section 5.4.2.3.

Compounds may include, but are not limited to, peptides such as, for example, soluble peptides, including but not limited to, Ig-tailed fusion peptides, and members of random peptide libraries; (see, *e.g.*, Lam, *et al.*, 1991, *Nature* 354:82-84; Houghten, *et al.*,

1991, *Nature* 354:84-86), and combinatorial chemistry-derived molecular library made of D- and/or L- configuration amino acids, phosphopeptides (including, but not limited to members of random or partially degenerate, directed phosphopeptide libraries; see, *e.g.*, Songyang, *et al.*, 1993, *Cell* 72:767-778), antibodies (including, but not limited to, polyclonal, monoclonal, humanized, anti-idiotypic, chimeric or single chain antibodies, and FAb, F(ab')<sub>2</sub> and FAb expression library fragments, and epitope-binding fragments thereof), and small organic or inorganic molecules.

Such compounds may further comprise compounds, in particular drugs or members of classes or families of drugs, known to ameliorate the symptoms of a condition, disorder, or disease involving cell death.

Such compounds include families of antidepressants such as lithium salts, carbamazepine, valproic acid, lysergic acid diethylamide (LSD), *p*-chlorophenylalanine, *p*-propyldopacetamide dithiocarbamate derivatives *e.g.*, FLA 63; anti-anxiety drugs, *e.g.*, diazepam; monoamine oxidase (MAO) inhibitors, *e.g.*, iproniazid, clorgyline, phenelzine and isocarboxazid; biogenic amine uptake blockers, *e.g.*, tricyclic antidepressants such as desipramine, imipramine and amitriptyline; serotonin reuptake inhibitors *e.g.*, fluoxetine; antipsychotic drugs such as phenothiazine derivatives (*e.g.*, chlorpromazine (thorazine) and trifluopromazine), butyrophenones (*e.g.*, haloperidol (Haldol)), thioxanthene derivatives (*e.g.*, chlorprothixene), and dibenzodiazepines (*e.g.*, clozapine); benzodiazepines; dopaminergic agonists and antagonists *e.g.*, L-DOPA, cocaine, amphetamine,  $\alpha$ -methyl-tyrosine, reserpine, tetrabenazine, benzotropine, pargyline; noradrenergic agonists and antagonists *e.g.*, clonidine, phenoxybenzamine, phentolamine, tropolone.

Compounds identified via assays such as those described herein may be useful, for example, in elaborating the biological function of protective sequence products and for ameliorating conditions, disorders, or diseases involving cell death. Assays for testing the effectiveness of compounds identified by, for example, techniques such as those described in Sections 5.4.2.1 - 5.4.2.3, are discussed, below, in Section 5.4.2.4.

#### 5.4.2.1 In Vitro Screening Assays for Compounds which Bind to Protective Sequence Products

5                    *In vitro* systems may be designed to identify compounds capable of binding the protective sequence products of the invention. Compounds identified may be useful, for example, in modulating the activity of unimpaired and/or mutant protective sequence products, may be useful in elaborating the biological function of the protective sequence product, may be utilized in screens for identifying compounds which disrupt normal  
10 protective sequence product interactions or may in themselves disrupt such interactions.

                  The principle of the assays used to identify compounds which bind to the protective sequence product involves preparing a reaction mixture of the protective sequence product and the test compound under conditions and for a time sufficient to allow the two components to interact and bind, thus forming a complex which can be removed and/or  
15 detected in the reaction mixture. These assays can be conducted in a variety of ways. For example, one method to conduct such an assay involves anchoring a protective sequence product or a test substance onto a solid support and detecting protective sequence product/test compound complexes formed on the solid support at the end of the reaction. In one embodiment of such a method, the protective sequence product may be anchored onto a solid  
20 support, and the test compound, which is not anchored, may be labeled, either directly or indirectly.

                  In practice, microtiter plates are conveniently utilized as the solid support. The anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished by simply coating the solid surface with a  
25 solution of the protein and drying. Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein to be immobilized may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

                  In order to conduct the assay, the non-immobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted  
30 components are removed (*e.g.*, by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the previously non-



immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the previously non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; *e.g.*, using a labeled antibody specific for the previously non-immobilized component (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody).

Alternatively, a reaction can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; *e.g.*, using an immobilized antibody specific for the protective sequence product or the test compound to anchor any complexes formed in solution, and a labeled antibody specific for the other component of the possible complex to detect anchored complexes.

#### 5.4.2.2 Assays for Proteins which Interact with Protective Sequence Products

Any method suitable for detecting protein-protein interactions may be employed for identifying protective sequence product-protein interactions.

Among the traditional methods that may be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns. Utilizing procedures such as these allows for the identification of proteins, including intracellular proteins, which interact with protective sequence products. Once isolated, such a protein can be identified and can be used in conjunction with standard techniques, to identify proteins it interacts with. For example, at least a portion of the amino acid sequence of a protein which interacts with the protective sequence product can be ascertained using techniques well known to those of skill in the art, such as via the Edman degradation technique (see, *e.g.*, Creighton, 1983, "Proteins: Structures and Molecular Principles," W.H. Freeman & Co., N.Y., pp.34-49). The amino acid sequence obtained may be used as a guide for the generation of oligonucleotide mixtures that can be used to screen for gene sequences encoding such proteins. Screening may be accomplished, for example, by standard hybridization or PCR techniques. Techniques for the generation of oligonucleotide mixtures and the screening are well known. (See, *e.g.*, Ausubel, *supra*, and 1990, "PCR

Protocols: A Guide to Methods and Applications," Innis, *et al.*, eds. Academic Press, Inc., New York).

Additionally, methods may be employed which result in the simultaneous identification of genes that encode a protein that interacts with a protective sequence product.

5 These methods include, for example, probing expression libraries with labeled protective sequence product, using the protective sequence product in a manner similar to the well-known technique of antibody probing of IgT11 libraries.

One method that detects protein interactions *in vivo*, the two-hybrid system, is described in detail for illustration only and not by way of limitation. One version of this  
10 system has been described (Chien, *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, 88:9578-9582) and is commercially available from Clontech (Palo Alto, CA).

Briefly, utilizing such a system, plasmids are constructed which encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the protective sequence product and the other consists of the transcription activator  
15 protein's activation domain fused to an unknown protein which is encoded by a cDNA which has been recombined into this plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (*e.g.*, HBS or *lacZ*) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate  
20 transcription of the reporter gene: the DNA-binding domain hybrid cannot because it does not provide activation function and the activation domain hybrid cannot because it cannot localize to the activator's binding sites. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product.

25 The two-hybrid system or related methodologies may be used to screen activation domain libraries for proteins that interact with the "bait" gene product. By way of example, and not by way of limitation, protective sequence products of the invention may be used as the bait gene product. Total genomic or cDNA sequences are fused to the DNA encoding an activation domain. This library and a plasmid encoding a hybrid of a bait  
30 protective sequence product fused to the DNA-binding domain are co-transformed into a yeast reporter strain, and the resulting transformants are screened for those which express the

reporter gene. For example, a bait protective sequence, such as the open reading frame of the gene, can be cloned into a vector such that it is translationally fused to the DNA encoding the DNA-binding domain of the GAL4 protein. These colonies are purified and the library plasmids responsible for reporter gene expression are isolated. DNA sequencing is then used to identify the proteins encoded by the library plasmids.

A cDNA library of the cell line, from which proteins which interact with bait protective sequence products are to be detected, can be made using methods routinely practiced in the art. According to the particular system described herein, for example, the cDNA fragments can be inserted into a vector such that they are translationally fused to the transcriptional activation domain of GAL4. Such a library can be co-transformed along with the bait protective sequence-GAL4 fusion plasmid into a yeast strain that contains a lacZ gene driven by a promoter that contains GAL4 activation sequence. A cDNA encoded protein, fused to a GAL4 transcriptional activation domain that interacts with bait protective sequence product will reconstitute an active GAL4 protein and thereby drive expression of the HIS3 gene. Colonies that express HIS3 can be detected by their growth on petri dishes containing semi-solid agar based media lacking histidine. The cDNA can then be purified from these strains, and used to produce and isolate the bait protective sequence product-interacting protein using techniques routinely practiced in the art.

#### **5.4.2.3 Assays for Compounds which Interfere with or Potentiate Protective Sequence Products Macromolecule Interaction**

The protective sequence products may, *in vivo*, interact with one or more macromolecules, including intracellular macromolecules, such as proteins. Such macromolecules may include, but are not limited to, nucleic acid molecules and those proteins identified via methods such as those described, above, in Sections 5.4.2.1 - 5.4.2.2. For purposes of this discussion, the macromolecules are referred to herein as "binding partners". Compounds that disrupt protective sequence product binding to a binding partner may be useful in regulating the activity of the protective sequence product, especially mutant protective sequence products. Such compounds may include, but are not limited to molecules such as peptides, and the like, as described, for example, in Section 5.4.2.1 above.

The basic principle of an assay system used to identify compounds which interfere with or potentiate the interaction between the protective sequence product and a binding partner or partners involves preparing a reaction mixture containing the protective sequence product and the binding partner under conditions and for a time sufficient to allow the two to interact and bind, thus forming a complex. In order to test a compound for inhibitory activity, the reaction mixture is prepared in the presence and absence of the test compound. The test compound may be initially included in the reaction mixture, or may be added at a time subsequent to the addition of protective sequence product and its binding partner. Control reaction mixtures are incubated without the test compound or with a compound that is known not to block complex formation. The formation of any complexes between the protective sequence product and the binding partner is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the protective sequence product and the binding partner. Additionally, complex formation within reaction mixtures containing the test compound and normal protective sequence product also may be compared to complex formation within reaction mixtures containing the test compound and a mutant protective sequence product. This comparison may be important in those cases wherein it is desirable to identify compounds that disrupt interactions of mutant but not normal protective sequence product.

In order to test a compound for potentiating activity, the reaction mixture is prepared in the presence and absence of the test compound. The test compound may be initially included in the reaction mixture, or may be added at a time subsequent to the addition of protective sequence product and its binding partner. Control reaction mixtures are incubated without the test compound or with a compound that is known not to block complex formation. The formation of any complexes between the protective sequence product and the binding partner is then detected. Increased formation of a complex in the reaction mixture containing the test compound, but not in the control reaction, indicates that the compound enhances and therefore potentiates the interaction of the protective sequence product and the binding partner. Additionally, complex formation within reaction mixtures containing the test compound and normal protective sequence product may also be compared to complex formation within reaction mixtures containing the test compound and a mutant protective

sequence product. This comparison may be important in those cases wherein it is desirable to identify compounds that enhance interactions of mutant but not normal protective sequence product.

5                   In alternative embodiments, the above assays may be performed using a reaction mixture containing the protective sequence product, a binding partner and a third compound which disrupts or enhances protective sequence product binding to the binding partner. The reaction mixture is prepared and incubated in the presence and absence of the test compound, as described above, and the formation of any complexes between the  
10                   protective sequence product and the binding partner is detected. In this embodiment, the formation of a complex in the reaction mixture containing the test compound, but not in the control reaction, indicates that the test compound interferes with the ability of the second compound to disrupt protective sequence product binding to its binding partner.

                  The assays for compounds that interfere with or potentiate the interaction of  
15                   the protective sequence products and binding partners can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the protective sequence product or the binding partner onto a solid support and detecting complexes formed on the solid support at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to  
20                   obtain different information about the compounds being tested. For example, test compounds which interfere with or potentiate the interaction between the protective sequence products and the binding partners, *e.g.*, by competition, can be identified by conducting the reaction in the presence of the test substance; *i.e.*, by adding the test substance to the reaction mixture prior to or simultaneously with the protective sequence product and interactive intracellular  
25                   binding partner. Alternatively, test compounds which disrupt preformed complexes, *e.g.*, compounds with higher binding constants which displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are described briefly below.

                  In a heterogeneous assay system, either the protective sequence product or the  
30                   interactive binding partner, is anchored onto a solid surface, while the non-anchored species is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized.

The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the protective sequence product or binding partner and drying. Alternatively, an immobilized antibody specific for the species to be anchored may be used to anchor the species to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the partner of the immobilized species is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (*e.g.*, by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized species is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized species is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface: *e.g.*, using a labeled antibody specific for the initially non-immobilized species (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; *e.g.*, using an immobilized antibody specific for one of the binding components to anchor any complexes formed in solution, and a labeled antibody specific for the other partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex formation or which disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the protective sequence product and the interactive binding partner is prepared in which either the protective sequence product or its binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, *e.g.*, U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the species from the preformed complex will result in the generation of a signal above

background. In this way, test substances that disrupt protective sequence product/binding partner interaction can be identified.

In another embodiment of the invention, these same techniques can be employed using peptide fragments which correspond to the binding domains of the protective sequence product and/or the binding partner (in cases where the binding partner is a protein), in place of one or both of the full length proteins. Any number of methods routinely practiced in the art can be used to identify and isolate the binding sites. These methods include, but are not limited to, mutagenesis of the gene encoding one of the proteins and screening for disruption of binding in a co-immunoprecipitation assay. Compensating mutations in the gene encoding the second species in the complex can then be selected. Sequence analysis of the genes encoding the respective proteins will reveal the mutations that correspond to the region of the protein involved in interactive binding. Alternatively, one protein can be anchored to a solid surface using methods described in this Section above, and allowed to interact with and bind to its labeled binding partner, which has been treated with a proteolytic enzyme, such as trypsin. After washing, a short, labeled peptide comprising the binding domain may remain associated with the solid material, which can be isolated and identified by amino acid sequencing. Also, once the gene coding for the segments is engineered to express peptide fragments of the protein, it can then be tested for binding activity and purified or synthesized.

For example, and not by way of limitation, a protective sequence product can be anchored to a solid material as described, above, in this Section by making a GST-1 fusion protein and allowing it to bind to glutathione agarose beads. The binding partner can be labeled with a radioactive isotope, such as  $^{35}\text{S}$ , and cleaved with a proteolytic enzyme such as trypsin. Cleavage products can then be added to the anchored GST-1 fusion protein and allowed to bind. After washing away unbound peptides, labeled bound material, representing the binding partner binding domain, can be eluted, purified and analyzed for amino acid sequence by well-known methods. Peptides so identified can be produced synthetically or produced using recombinant DNA technology.

#### 5.4.2.4 Assays for the Identification of Compounds which Modulate Conditions, Disorders, or Diseases Involving Cell Death

5                   Compounds, including, but not limited to, binding compounds identified via assay techniques such as those described, above, in Sections 5.4.2.1 - 5.4.2.3, can be tested for the ability to ameliorate symptoms of a condition, disorder, or disease involving cell death.

10                   It should be noted that the assays described herein can be used to identify compounds which affect activity by either affecting protective sequence expression or by affecting the level of protective sequence product activity. For example, compounds may be identified which are involved in another step in the pathway in which the protective sequence and/or protective sequence product is involved, such as, for example, a step which is either "upstream" or "downstream" of the step in the pathway mediated by the protective sequence.

15                   Such compounds may, by affecting this same pathway, modulate the effect on the development of conditions, disorders, or diseases involving cell death. Such compounds can be used as part of a therapeutic method for the treatment of the condition, disorder, or disease.

                  Described below are cell-based and animal model-based assays for the identification of compounds exhibiting such an ability to ameliorate symptoms of a condition, disorder, or disease involving cell death.

20

                  First, cell-based systems can be used to identify compounds which may act to ameliorate symptoms of a condition, disorder, or disease, including, but not limited to, those described in Section 5.4.1.1. Such cell systems can include, for example, recombinant or non-recombinant cell, such as cell lines, which express the protective sequence of interest.

25                   In utilizing such cell systems, cells which express the protective sequence of interest may be exposed to a compound suspected of exhibiting an ability to ameliorate symptoms of a condition, disorder, or disease involving cell death at a sufficient concentration and for a sufficient time to elicit such an amelioration of such symptoms in the exposed cells. After exposure, the cells can be assayed to measure alterations in the expression of the protective sequence, *e.g.*, by assaying cell lysates for cerebral mRNA transcripts (*e.g.*, by Northern analysis) or for protective sequence products expressed by the cell; compounds which modulate expression of the protective sequence are good candidates

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as therapeutics.

In addition, animal-based systems or models for a condition, disorder, or disease involving cell death, for example, transgenic mice containing a human or altered form of a protective sequence, may be used to identify compounds capable of ameliorating symptoms of the condition, disorder, or disease. Such animal models may be used as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions. For example, animal models may be exposed to a compound suspected of exhibiting an ability to ameliorate symptoms, at a sufficient concentration and for a sufficient time to elicit such an amelioration of symptoms of a condition, disorder, or disease involving cell death. The response of the animals to the exposure may be monitored by assessing the reversal of the symptoms of the condition, disorder, or disease.

With regard to intervention, any treatments that reverse any aspect of symptoms of a condition, disorder, or disease involving cell death, should be considered as candidates for human therapeutic intervention in such conditions, disorders, or diseases.

Dosages of test agents may be determined by deriving dose-response curves, as discussed in Section 5.5.1, below.

#### **5.4.3 Additional Uses for the Protective Sequences, Protective Sequence Products, or Their Regulatory Elements**

In addition to the uses described above, the polynucleotides of the present invention can be used for various other purposes. For example, they can be used to express recombinant protein for analysis, characterization or therapeutic use; as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic conditions, disorders, or diseases; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response.

The proteins provided by the present invention can similarly be used to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

## 5.5 Pharmaceutical Preparations and Methods of Administration

The compounds which are determined to affect protective sequence expression or gene product activity can be administered to a patient at therapeutically effective doses to treat or ameliorate a condition, disorder, or disease involving cell death or modulate a cell death-related process described herein. A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms of such a condition, disorder, or disease.

### 5.5.1 Effective Dose

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD<sub>50</sub>/ED<sub>50</sub>.

Compounds that exhibit large therapeutic indices are preferred. While compounds which exhibit toxic side effects may be used, care should be taken to design a delivery system which targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

5           The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the  $ED_{50}$  with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the  
10           invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range which includes the  $IC_{50}$  (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in  
15           plasma may be measured, for example, by high performance liquid chromatography.

          As defined herein, a therapeutically effective amount of antibody, protein, or polypeptide (*i.e.*, an effective dosage) ranges from about 0.001 to 30 mg/kg body weight, preferably about 0.01 to 25 mg/kg body weight, more preferably about 0.1 to 20 mg/kg body weight, and even more preferably about 1 to 10 mg/kg, 2 to 9 mg/kg, 3 to 8 mg/kg, 4 to 7  
20           mg/kg, or 5 to 6 mg/kg body weight.

          The skilled artisan will appreciate that certain factors may influence the dosage required to effectively treat a subject, including but not limited to the severity of the disease or condition, disorder, or disease, previous treatments, the general health and/or age of the subject, and other diseases present. Moreover, treatment of a subject with a therapeutically  
25           effective amount of a protein, polypeptide, or antibody can include a single treatment or, preferably, can include a series of treatments. In a preferred example, a subject is treated with antibody, protein, or polypeptide in the range of between about 0.1 to 20 mg/kg body weight, one time per week for between about 1 to 10 weeks, preferably between 2 to 8 weeks, more preferably between about 3 to 7 weeks, and even more preferably for about 4, 5, or 6 weeks.  
30           It will also be appreciated that the effective dosage of antibody, protein, or polypeptide used for treatment may increase or decrease over the course of a particular treatment. Changes in

dosage may result and become apparent from the results of diagnostic assays as described herein.

### 5.5.2 Formulations and Use

5           Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients.

          Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral rectal or topical administration.

          For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (*e.g.*, pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (*e.g.*, lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (*e.g.*, magnesium stearate, talc or silica); disintegrants (*e.g.*, potato starch or sodium starch glycolate); or wetting agents (*e.g.*, sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (*e.g.*, sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (*e.g.*, lecithin or acacia); non-aqueous vehicles (*e.g.*, almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (*e.g.*, methyl or propyl-  
p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

          Preparations for oral administration may be suitably formulated to give controlled release of the active compound.

          For buccal administration the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides.

In certain embodiments, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment. This may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, *e.g.*, in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. In one embodiment, administration can be by direct injection at the site (or former site) of a malignant tumor or neoplastic or pre-neoplastic tissue.

For topical application, the compounds may be combined with a carrier so that an effective dosage is delivered, based on the desired activity.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection.

Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

The compositions may, if desired, be presented in a pack or dispenser device that may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

## **EXAMPLE: SEQUENCE AND CHARACTERIZATION OF PROTECTIVE SEQUENCES**

In the example presented herein, the sequence and characterization of the protective sequences are provided.

### **6.1 Materials and Methods**

#### **6.1.1 Preparation of DNA**

A human fetal brain cDNA library (Gibco), in which individual clones were inserted into the NotI-SalI site of the pCMV-SPORT2 vector, was diluted 200,000 fold in LB broth (DIFCO Laboratories) containing 0.2 mg/ml ampicillin (Sigma). The diluted library (100-140  $\mu$ l) was then plated and grown on LB agar (DIFCO Laboratories) bioassay plates with 0.2 mg/ml ampicillin. Plates were incubated at 37°C for 24 hours. Single colonies were then used to inoculate deep-well blocks containing 1.5 ml LB broth containing 0.2 mg/ml ampicillin. Inoculated cultures were incubated at 37°C with agitation at 150-200 rpm for 18-24 hours. Replicate plates were created from the cultures by adding 20  $\mu$ l of culture to 80  $\mu$ l of LB broth containing 18% glycerol and 0.2 mg/ml ampicillin and stored at -80°C. Remaining bacterial cells were centrifuged at 1000 x g for 6 minutes to collect the cells at the bottom. Following centrifugation, the broth was decanted off of the bacterial pellet and the pellet resuspended and then stored in 100  $\mu$ l of Cell Resuspension Solution (Promega) at 4°C for up to one week.

Plasmid DNA was extracted using Promega MagneSil kits with a modified protocol. The pelleted bacteria were re-suspended and 50  $\mu$ l was transferred into a round bottom plate that rests on a magnet. Cell Lysis Solution (50  $\mu$ l) was added and the plate was incubated at room temperature without agitation for 30 seconds. Following lysis, 70  $\mu$ l of a Neutralization Solution/MagneSil Paramagnetic Particles mixture (pre-mixed at a ratio of

6:1) was added. The reaction was mixed by pipetting and incubated at room temperature without agitation for 5 minutes to allow the magnetic particles to be drawn to the magnet. The supernatant containing plasmid DNA was then transferred to a new plate and stored at -20°C.

Individual clones were chosen for their ability to delay or prevent cell death when introduced into a cell predisposed to undergoing cell death, relative to a corresponding cell into which no exogenous protective sequence had been introduced.

### **6.1.2 Sequence Characterization of the DNA**

The cDNA inserts of the clonally pure plasmids which are selected for their ability to protect cells from cell death when introduced into cells predisposed to undergo cell death are sequenced using the ABI Big Dye terminator Cycle Sequencing Ready Reaction Kit and subsequently analyzed on the ABI310 capillary sequencing machine (PE Biosystems, Foster City, CA).

Briefly, 0.5 mg of plasmid DNA is mixed with 3.2 pmole of either the M13 forward (5'-TGTAACGACGGCCAGT-3'; SEQ ID NO:465) or the M13 reverse (5'-CAGGAAACAGCTATGACC-3'; SEQ ID NO:466) sequencing primer and 8 ml of the terminator ready reaction mix in a total volume of 20 ml. The cycle sequencing reaction is carried out in a thermocycler (PCR machine) using standard methods known by those skilled in the art. The extension products from the sequencing reaction are purified by precipitation using isopropanol. 80 ml of 75% isopropanol is added to the sample and after thorough mixing, the sample is incubated at room temperature (25°C) for 20 minutes. The sample is then centrifuged at 12,000 x g for 20 minutes at room temperature. The supernatant is removed and the pellet is rinsed once by addition of 250 ml of 75% isopropanol followed by centrifugation as above for 5 minutes. The supernatant is removed and the sample air-dried for 10 minutes. The sample is then resuspended in 20 ml of TSR (template suppression reagent) and denatured by heating at 94°C for 2 minutes and rapidly cooling on ice. The subsequent electrophoresis and analysis is carried out on the ABI310 sequencer according to the manufacturer's protocol. The entire cDNA clone is similarly sequenced by the use of sequence specific internal primers as required.

### 6.1.3 Sequence Comparison

The sequence data for the protective cDNA clones is compared using the BLAST 2.0 algorithm (Altschul, SF *et al.*, 1997, Nuc. Acids Res. 25:3389) against known sequences in the GeneBank sequence database maintained by NCBI (National Center for Biotechnology Information). This program uses the two-hit method to find homology within the database. The BLAST nucleotide searches are performed with the "BLAST N" program (wordlength = 11) to obtain nucleic acids homologous to nucleic acid molecules of the invention. BLAST protein searches of potential ORFs are performed with the "BLAST P" program (wordlength = 3) to obtain amino acid sequences homologous to the ORFs of the invention.

### 6.1.4 Immuno-Cytochemistry Protocol for the Characterization of Protected Cells

Transfected tissue is immersed in freshly prepared 2.5% paraformaldehyde (PFA) in phosphate buffered saline (PBS) for two hours to fix the tissue. PFA is removed by aspiration and the fixed tissue washed consecutively four times in PBS for 15 minutes, changing the PBS solution between each wash. Upon removal of the final PBS wash, the tissue is immersed in a blocking solution consisting of 10% goat serum, 2% bovine serum albumin (BSA), and 0.25% Triton X-100 for a duration of two hours.

After removal of the blocking solution, the tissue is immersed in a primary antibody solution, freshly prepared by adding rabbit anti-GFP polyclonal (1:2000 ul) into blocking solution, for an incubation period of twelve hours at 4°C.

After removal of the primary antibody solution, the tissue is washed consecutively four times in PBS for 10 minutes, changing the PBS solution between each wash. An anti-rabbit, fluorescently conjugated secondary antibody, diluted in PBS at a concentration of 1:500, is then added to the tissue and allowed to incubate at room temperature for four hours. The secondary antibody solution is removed by aspiration and the tissue washed consecutively four times in PBS for 15 minutes, changing the PBS solution between each wash. After the final wash is removed, the tissue is mounted on glass slides and dried at 37°C for thirty minutes. A three-minute xylene incubation is performed before the addition of coverslips to preserve the slices.



## 6.2 Results

The following protective sequences, which were obtained using the methods described in Section 6.1, were chosen based on their ability to prevent, delay, or rescue cells predisposed to undergo cell death, relative to a corresponding cell into which no exogenous protective sequence had been introduced.

### 6.2.1 Protective sequence CNI-00718

Protective sequence CNI-00718 (SEQ. ID NO:1) is a completely novel sequence which comprises 1794 nucleotides. Twenty-eight (28) potential ORFs have been identified within the protective sequence and are depicted in Table 2. The longest ORF is 112 amino acids. BLAST sequence comparison analysis of CNI-00718 against known nucleotide and protein sequences in the GenBank database reveals no significant homology at either the nucleotide or the amino acid level. As shown in Figure 3F, CNI-00718 caused about a 20-fold increase in the number of surviving neurons in stroked rat cortical brain slices compared to negative control slices which were exposed to EGFP with no protective sequence.

### 6.2.2 Protective sequence CNI-00722

Protective sequence CNI-00722 (SEQ. ID NO:58) comprises 810 nucleotides. Twelve (12) potential ORFs have been identified within the protective sequence and are depicted in Table 3. The longest ORF of the cDNA encodes 44 amino acids. BLAST sequence comparison analysis of CNI-00722 against known nucleic acids in the GenBank database reveals homology with the sequence encoding the human chromosome 16 BAC clone CIT987-SKA-113A6 (ACC. No. AC002299). At the nucleotide level, the overall percent homology between CNI-00722 and CIT987-SKA-113A6 is 99.6% (783/785 bases). CIT987-SKA-113A6 is an unidentified DNA. As shown in Figure 3F, CNI-00722 caused about a 21-fold increase in the number of surviving neurons in stroked rat cortical brain slices compared to negative control slices which were exposed to EGFP with no protective sequence.

### 6.2.3 Protective sequence CNI-00725

Protective sequence CNI-00725 (SEQ. ID NO:83) comprises 920 nucleotides.

Eleven (11) potential ORFs have been identified within the protective sequence and are depicted in Table 4. BLAST sequence comparison analysis of CNI-00725 against known nucleic acids in the GenBank database reveals a 97% identity (870/897 bases) with a human mitochondrial sequence encoding the 16S rRNA and tRNA for the amino acid Leucine (ACC. No. V00710). However, most of the homology (95%) is with the 16S rRNA sequence. As shown in Figure 3F, CNI-00725 caused about a 14-fold increase in the number of surviving neurons in stroked rat cortical brain slices compared to negative control slices which were exposed to EGFP with no protective sequence.

### 6.2.4 Protective sequence CNI-00726

Protective sequence CNI-00726 (SEQ. ID NO:106) comprises 2144

nucleotides. Twenty-six (26) potential ORFs have been identified within the protective sequence and are depicted in Table 5. The longest ORF of CNI-00726 encodes 147 amino acids. BLAST sequence comparison analysis of CNI-00726 against known nucleic acids in the GenBank database reveals a 99.7% identity (1820/1825 bases) with the human ubiquitin-conjugating enzyme variant 1, UBE2V1 (ACC No. NM\_003349); a 99.6% identity (1820/1826 bases) with the human DNA-binding protein CROC-1A (ACC No. U39360); and a 72.5% identity (401/553 bases) with the human MMS2 protein (ACC No. AF049140). At the protein level, CNI-00726 has a 100% identity with the 80-221 amino acid region of UBE2VI; a 97% identity (136/140 amino acids) with the 31-170 amino acid region of CROC-1A; and a 90% identity (132/147 amino acids) with the human MMS2 protein. The enzyme UBE2V1 may be involved in controlling differentiation by affecting the distribution of cells in different phases during the cell cycle (Sancho, *et al.* 1998, *Mol. Cell. Biol.* 18: 576-89). The protein CROC-1A is capable of transcriptionally activating the FOS promoter (Rothofsky & Lin, 1997, *Gene* 195: 141-9; Lin & Rothofsky, U.S. Patent No. 5,736,331). As shown in Figure 3F, CNI-00726 caused about a 19-fold increase in the number of surviving neurons in stroked rat cortical brain slices compared to negative control slices which were exposed to EGFP with no protective sequence.

### 6.2.5 Protective sequence CNI-00727

Protective sequence CNI-00727 (SEQ. ID NO:159) is a completely novel sequence which comprises 1293 nucleotides. Nineteen (19) potential ORFs have been identified within the protective sequence and are depicted in Table 6. The longest ORF is 54 amino acids. BLAST sequence comparison analysis of CNI-00727 against known nucleotide and protein sequences in the GenBank database reveals no significant homology at either the nucleotide or the amino acid level. As shown in Figure 3F, CNI-00727 caused about a 17-fold increase in the number of surviving neurons in stroked rat cortical brain slices compared to negative control slices which were exposed to EGFP with no protective sequence.

### 6.2.6 Protective sequence CNI-00728

Protective sequence CNI-00728 (SEQ. ID NO:198) comprises 1466 nucleotides. Twenty-four (24) potential ORFs have been identified within the protective sequence and are depicted in Table 7. The longest ORF is 59 amino acids. BLAST sequence comparison analysis of CNI-00728 against known nucleic acids in the GenBank database reveals a 99.9% identity (1342/1343 bases) with the 3' untranslated region of human sorting nexin 10 mRNA (ACC. No. AF121860). As shown in Figure 3F, CNI-00728 caused about a 10-fold increase in the number of surviving neurons in stroked rat cortical brain slices compared to negative control slices which were exposed to EGFP with no protective sequence.

### 6.2.7 Protective sequence CNI-00729

Protective sequence CNI-00729 (SEQ. ID NO:247) comprises 1659 nucleotides. Twenty-two (22) potential ORFs have been identified within the protective sequence and are depicted in Table 8. BLAST sequence comparison analysis of CNI-00729 against known nucleic acids in the GenBank database reveals a 99.9% identity (1611/1612 bases) with a human actin binding protein, p57 (ACC No. D44497); a 99.9% identity (1561/1562 bp) with human coronin (ACC No. X89109); and a 99.7% identity (1585/1589 bp) with human coronin-like protein, HCORO1 (ACC No. U34690). At the amino acid level, CNI-00729 is identical to human actin protein, p57; identical to human coronin; and 99% identical (459/461 aa) with human coronin-like protein (Suzuki, Jpn. Kokai Tokyo Koho Patent No. 96119996). The p57 protein is an actin-binding protein and a member of the

coronin family of proteins. The coronins are proteins involved in cell locomotion, cytokinesis, and actin-mediated cellular processes such as phagocytosis (deHostos, 1999, *Trends Cell Biol.* 9: 345-50). As shown in Figure 3F, CNI-00729 caused about a 13-fold increase in the number of surviving neurons in stroked rat cortical brain slices compared to negative control slices which were exposed to EGFP with no protective sequence.

#### 6.2.8 Protective sequence CNI-00730

Protective sequence CNI-00730 (SEQ. ID NO:292) comprises 722 nucleotides. Nine (9) potential ORFs have been identified within the protective sequence and are depicted in Table 9. The longest ORF of the cDNA encodes 142 amino acids. BLAST sequence comparison analysis of CNI-00730 against known nucleic acids in the GenBank database reveals homology with the sequence encoding human mitochondrial ATP synthase, F0 complex, subunit 9 (ACC. No. NM\_001689). At the nucleotide level, the overall percent homology between CNI-00730 and human mitochondrial ATP synthase, F0 complex, subunit 9 is 99.4% (651/655 bp). At the amino acid level, the CNI-00730 and human mitochondrial ATP synthase, F0 complex, subunit 9 proteins are identical. There are three reported genes (P1, P2, and P3) that encode identical forms of mature human mitochondrial ATP synthase, F0 complex, subunit 9; CNI-00730 is homologous to the P3 gene (Yan, *et al.* 1994, *Genomics* 24: 375-7). Subunit 9 accumulates in the lysosomes of individuals affected with the juvenile and late-infantile forms of neuronal ceroid lipofuscinosis (Batten disease) (Tanner, *et al.*, 1997, *Biochim. Biophys. Acta* 1361: 251-62). As shown in Figure 3F, CNI-00730 caused about a 14-fold increase in the number of surviving neurons in stroked rat cortical brain slices compared to negative control slices which were exposed to EGFP with no protective sequence.

#### 6.2.9 Protective sequence CNI-00731

Protective sequence CNI-00731 (SEQ. ID NO:311) comprises 364 nucleotides. Seven (7) potential ORFs have been identified within the protective sequence and are depicted in Table 10. The longest ORF is 32 amino acids. BLAST sequence comparison analysis of CNI-00731 against known nucleic acids in the GenBank database reveals a 98.5% identity (322/326 bases) with the 3' untranslated region of human interferon-

induced cellular resistance mediator protein (MxA) mRNA (ACC. No. M30817). As shown in Figure 3F, CNI-00731 caused about an 11-fold increase in the number of surviving neurons in stroked rat cortical brain slices compared to negative control slices which were exposed to EGFP with no protective sequence.

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#### 6.2.10 Protective sequence CNI-00732

Protective sequence CNI-00732 (SEQ. ID NO:326) comprises 1046 nucleotides. Eight (8) potential ORFs have been identified within the protective sequence and are depicted in Table 11. The longest ORF is 50 amino acids. BLAST sequence comparison analysis of CNI-00732 against known nucleic acids in the GenBank database reveals a 94% identity (949/1013 bases) with a human mitochondrial sequence encoding the 12S rRNA and tRNA for the amino acid Valine (ACC. No. V00710). However, most of the homology (97%) is with the 12S rRNA sequence. As shown in Figure 3F, CNI-00732 caused about a 12-fold increase in the number of surviving neurons in stroked rat cortical brain slices compared to negative control slices which were exposed to EGFP with no protective sequence.

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#### 7 DEPOSIT OF DNA

The following DNA clones were deposited with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure, and comply with the criteria set forth in 37 C.F.R. § 1.801-1.809 regarding availability and permanency of deposits. The deposits were made on the date indicated and assigned the indicated accession number:

25

<u>Microorganism Deposit</u>	<u>ATCC Deposit No.</u>	<u>Date of Deposit</u>
CNI-NPP2-CP10	PTA-1492	March 16, 2000

CNI-NPP2-CP10 represents a composite deposit of a mixture of ten (10) DNA clones. To distinguish and isolate each of the individual DNA, a sample of the DNA preparation can be digested with *Not* I and *Sal* I, and the resulting products can be separated

30

by standard gel electrophoresis techniques using a 1% agarose gel in TAE buffer. Liberated inserts are of the following approximate sizes:

	1:	CNI-00718	1794 bp
	2:	CNI-00722	810 bp
5	3:	CNI-00725	920 bp
	4:	CNI-00726	2144 bp
	5:	CNI-00727	1293 bp
	6:	CNI-00728	1466 bp
	7:	CNI-00729	1659 bp
10	8:	CNI-00730	722 bp
	9:	CNI-00731	364 bp
	10:	CNI-00732	1046 bp

#### 8 REFERENCES CITED

15 The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing  
20 description and accompanying drawings.

All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be  
25 incorporated by reference.

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a polypeptide comprising:

- 5 (a) an amino acid sequence shown in Figures 4(A-AB);
- (b) an amino acid sequence shown in Figures 5(A-L);
- (c) an amino acid sequence shown in Figures 6(A-K);
- (d) an amino acid sequence shown in Figures 7(A-Z);
- (e) an amino acid sequence shown in Figures 8(A-S);
- 10 (f) an amino acid sequence shown in Figures 9(A-X);
- (g) an amino acid sequence shown in Figures 10(A-V);
- (h) an amino acid sequence shown in Figures 11(A-I);
- (i) an amino acid sequence shown in Figures 12(A-G); or
- (j) the amino acid sequence shown in Figure 13(A-H).

15

2. An isolated nucleic acid molecule comprising:

- (a) a nucleic acid sequence shown in Figures 4(A-AB);
- (b) a nucleic acid sequence shown in Figures 5(A-L);
- (c) a nucleic acid sequence shown in Figures 6(A-K);
- 20 (d) a nucleic acid sequence shown in Figures 7(A-Z);
- (e) a nucleic acid sequence shown in Figures 8(A-S);
- (f) a nucleic acid sequence shown in Figures 9(A-X);
- (g) a nucleic acid sequence shown in Figures 10(A-V);
- (h) a nucleic acid sequence shown in Figures 11(A-I);
- 25 (i) a nucleic acid sequence shown in Figures 12(A-G);
- (j) a nucleic acid sequence shown in Figure 13 (A-H); or
- (k) a nucleic acid sequence shown in Figures 1(A-J).

3. An isolated nucleic acid molecule comprising a complement of the nucleic acid molecule of any one of Claims 1 and 2.

30

4. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of Claim 3 under highly stringent conditions.
5. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of Claim 3 under moderately stringent conditions.
6. The isolated nucleic acid molecule of Claim 4, wherein said isolated nucleic acid molecule encodes a protective sequence product.
7. The isolated nucleic acid molecule of Claim 5, wherein said isolated nucleic acid molecule encodes a protective sequence product.
8. A vector comprising the nucleic acid of any one of Claims 1 and 2.
9. The vector of claim 8, wherein said vector is a viral vector.
10. An expression vector comprising the nucleic acid of any one of Claims 1 and 2 operatively associated with a regulatory nucleic acid controlling the expression of the nucleic acid in a host cell.
11. A host cell genetically engineered to contain the nucleic acid of any one of Claims 1 and 2.
12. A host cell genetically engineered to express the nucleic acid of any one of Claims 1 and 2 operatively associated with a regulatory nucleic acid controlling expression of the nucleic acid in said host cell.
13. The host cell of Claim 12, wherein said host cell is a neuronal cell.
14. The host cell of Claim 13, wherein said neuronal cell is a PC-12 cell or a primary dissociated neuron.



15. A transgenic, non-human animal which has been genetically engineered to contain a transgene comprising the nucleic acid of any one of Claims 1 and 2.

5 16. The transgenic, non-human animal of Claim 15, wherein the transgene is expressed.

17. An isolated polypeptide comprising:

10 (a) an amino acid sequence shown in Figures 4(A-AB);

(b) an amino acid sequence shown in Figures 5(A-L);

(c) an amino acid sequence shown in Figures 6(A-K);

(d) an amino acid sequence shown in Figures 7(A-Z);

(e) an amino acid sequence shown in Figures 8(A-S);

(f) an amino acid sequence shown in Figures 9(A-X);

(g) an amino acid sequence shown in Figures 10(A-V);

15 (h) an amino acid sequence shown in Figures 11(A-I);

(i) an amino acid sequence shown in Figures 12(A-G); or

(j) the amino acid sequence shown in Figure 13(A-H).

18. An isolated polypeptide comprising an amino acid sequence encoded by the  
20 isolated nucleic acid molecule of Claim 4.

19. An isolated polypeptide comprising an amino acid sequence encoded by the isolated nucleic acid molecule of Claim 5.

25 20. An isolated fusion polypeptide comprising a fusion peptide and an amino acid sequence comprising:

(a) an amino acid sequence shown in Figures 4(A-AB);

(b) an amino acid sequence shown in Figures 5(A-L);

(c) an amino acid sequence shown in Figures 6(A-K);

30 (d) an amino acid sequence shown in Figures 7(A-Z);

(e) an amino acid sequence shown in Figures 8(A-S);

- (f) an amino acid sequence shown in Figures 9(A-X);
- (g) an amino acid sequence shown in Figures 10(A-V);
- (h) an amino acid sequence shown in Figures 11(A-I);
- (i) an amino acid sequence shown in Figures 12(A-G); or
- (j) the amino acid sequence shown in Figure 13(A-H).

5

21. An isolated fusion polypeptide comprising a fusion peptide and an amino acid sequence encoded by the isolated nucleic acid molecule of Claim 4.

10

22. An isolated fusion polypeptide comprising a fusion peptide and an amino acid sequence encoded by the isolated nucleic acid molecules of Claim 5.

23. An antibody which binds to the isolated polypeptide of Claim 17.

15

24. A method for diagnosing a protective sequence-mediated condition, disorder or disease in an individual comprising obtaining a biological sample from said individual; contacting said biological sample with the antibody according to claim 23; wherein if said antibody interacts with said biological sample, but does not interact with a biological sample from a control individual not undergoing a protective sequence-mediated condition, disorder or disease, then a protective sequence-mediated condition, disorder or disease has been diagnosed.

20

25. A diagnostic kit for detecting a protective sequence-mediated condition, disorder or disease in an individual comprising a reagent in suitable packaging, wherein said reagent comprises the antibody according to claim 23.

25

26. A method for treating, ameliorating or preventing a protective sequence-mediated condition, disorder or disease in an individual comprising administering to the individual a compound which modulates the function, activity, expression and/or level of a protective sequence in a cell, cells, tissue, organ, organism or individual.

30

27. The method of Claim 26, wherein the compound inhibits the function, activity, expression and/or level of a protective sequence in a cell, cells, tissue, organ, organism or individual.

5           28. The method of Claim 26, wherein the compound enhances or potentiates the function, activity, expression and/or level of a protective sequence in a cell, cells, tissue, organ, organism or individual.

10           29. The methods of any one of Claims 26-28, wherein the compound is selected from the group consisting of a small organic molecule, an antibody, a ribozyme, an antisense molecule, and combinations thereof.

15           30. The method of any one of Claims 26-28, wherein the protective sequence-mediated condition, disorder, or disease is a condition, disorder, or disease of the central nervous system.

          31. The method of Claim 30, wherein the central nervous system condition is an ischemia-related condition.

20           32. The method of Claim 31, wherein the central nervous system condition is a stroke.

          33. The method of Claim 26, wherein the protective sequence encodes a polypeptide comprising:

- 25           (a) an amino acid sequence shown in Figures 4(A-AB);  
             (b) an amino acid sequence shown in Figures 5(A-L);  
             (c) an amino acid sequence shown in Figures 6(A-K);  
             (d) an amino acid sequence shown in Figures 7(A-Z);  
             (e) an amino acid sequence shown in Figures 8(A-S);  
30           (f) an amino acid sequence shown in Figures 9(A-X);  
             (g) an amino acid sequence shown in Figures 10(A-V);

- (h) an amino acid sequence shown in Figures 11(A-I);
- (i) an amino acid sequence shown in Figures 12(A-G); or
- (j) the amino acid sequence shown in Figure 13(A-H).

5           34.    The method of Claim 26, wherein the individual is a mammal.

          35.    The method of Claim 34, wherein the mammal is a human.

          36.    A method for treating, ameliorating, or preventing a protective sequence-  
10 mediated condition, disorder or disease in an individual comprising administering to the  
individual a compound which modulates the expression or activity of a protective sequence  
product and/or protective sequence regulatory product in the individual.

          37.    The method of Claim 36, wherein the compound inhibits the expression or  
15 activity of a protective sequence product and/or protective sequence regulatory product in the  
individual.

          38.    The method of Claim 36, wherein the compound enhances or potentiates the  
expression or activity of a protective sequence product and/or protective sequence regulatory  
20 product in the individual.

          39.    The method of Claim 36, wherein the compound is selected from the group  
consisting of a small organic molecule, an antibody, a ribozyme, an antisense molecule, and  
combinations thereof.

25

          40.    The method of Claim 36, wherein the protective sequence-mediated condition,  
disorder, or disease is a condition, disorder, or disease of the central nervous system.

          41.    The method of Claim 40, wherein the central nervous system condition is an  
30 ischemia-related condition.

42. The method of Claim 41, wherein the central nervous system condition is a stroke.

43. The method of Claim 36, wherein the protective sequence product comprises:

- (a) an amino acid sequence shown in Figures 4(A-AB);
- (b) an amino acid sequence shown in Figures 5(A-L);
- (c) an amino acid sequence shown in Figures 6(A-K);
- (d) an amino acid sequence shown in Figures 7(A-Z);
- (e) an amino acid sequence shown in Figures 8(A-S);
- (f) an amino acid sequence shown in Figures 9(A-X);
- (g) an amino acid sequence shown in Figures 10(A-V);
- (h) an amino acid sequence shown in Figures 11(A-I);
- (i) an amino acid sequence shown in Figures 12(A-G); or
- (j) the amino acid sequence shown in Figure 13(A-H).

44. The method of Claim 36, wherein the individual is a mammal.

45. The method of Claim 44, wherein the mammal is a human.

46. A method for identifying a compound which modulates expression of a protective sequence comprising:

- (a) contacting a test compound to a cell that expresses a protective sequence;
- (b) measuring a level of protective sequence expression in the cell;
- (c) comparing the level of protective sequence expression in the cell in the

presence of the test compound to a level of protective sequence expression in the cell in the absence of the test compound,

wherein if the level of protective sequence expression in the cell in the presence of the test compound differs from the level of expression of the protective sequence in the cell in the absence of the test compound, a compound that modulates expression of a protective sequence is identified.

47. The method of Claim 46, wherein the protective sequence is endogenously expressed within the cell.

48. The method of Claim 46, wherein the protective sequence encodes a polypeptide comprising:
- (a) an amino acid sequence shown in Figures 4(A-AB);
  - (b) an amino acid sequence shown in Figures 5(A-L);
  - (c) an amino acid sequence shown in Figures 6(A-K);
  - (d) an amino acid sequence shown in Figures 7(A-Z);
  - 10 (e) an amino acid sequence shown in Figures 8(A-S);
  - (f) an amino acid sequence shown in Figures 9(A-X);
  - (g) an amino acid sequence shown in Figures 10(A-V);
  - (h) an amino acid sequence shown in Figures 11(A-I);
  - (i) an amino acid sequence shown in Figures 12(A-G); or
  - 15 (j) the amino acid sequence shown in Figure 13(A-H).

49. The method of Claim 46, wherein the protective sequence comprises:
- (a) a nucleic acid sequence shown in Figures 4(A-AB);
  - (b) a nucleic acid sequence shown in Figures 5(A-L);
  - 20 (c) a nucleic acid sequence shown in Figures 6(A-K);
  - (d) a nucleic acid sequence shown in Figures 7(A-Z);
  - (e) a nucleic acid sequence shown in Figures 8(A-S);
  - (f) a nucleic acid sequence shown in Figures 9(A-X);
  - (g) a nucleic acid sequence shown in Figures 10(A-V);
  - 25 (h) a nucleic acid sequence shown in Figures 11(A-I);
  - (i) a nucleic acid sequence shown in Figures 12(A-G);
  - (j) a nucleic acid sequence shown in Figure 13 (A-H); or
  - (k) a nucleic acid sequence shown in Figures 1(A-J).

50. A method for identifying a compound which modulates expression, function or activity of a protective sequence product or protective sequence regulatory element comprising:

(a) contacting a test compound to a cell that expresses a protective sequence product or protective sequence regulatory element;

(b) measuring a level of protective sequence product or protective sequence regulatory element expression, function or activity in the cell;

(c) comparing the level of protective sequence product or protective sequence regulatory element expression, function or activity in the cell in the presence of the test compound to a level of protective sequence product or protective sequence regulatory element expression or activity in the cell in the absence of the test compound, wherein if the level of protective sequence product or protective sequence regulatory element expression, function or activity in the cell in the presence of the test compound differs from the level of protective sequence product or protective sequence regulatory element expression, function or activity in the cell in the absence of the test compound, a compound that modulates expression or activity of a protective sequence product or protective sequence regulatory element is identified.

51. The method of Claim 50, wherein the protective sequence product or protective sequence regulatory element comprises:

(a) an amino acid sequence shown in Figures 4(A-AB);

(b) an amino acid sequence shown in Figures 5(A-L);

(c) an amino acid sequence shown in Figures 6(A-K);

(d) an amino acid sequence shown in Figures 7(A-Z);

(e) an amino acid sequence shown in Figures 8(A-S);

(f) an amino acid sequence shown in Figures 9(A-X);

(g) an amino acid sequence shown in Figures 10(A-V);

(h) an amino acid sequence shown in Figures 11(A-I);

(i) an amino acid sequence shown in Figures 12(A-G); or

(j) the amino acid sequence shown in Figure 13(A-H).

52. A method for transferring a protective sequence into a cell comprising contacting the cell with a nucleic acid comprising a protective sequence such that the protective sequence is transferred into the cell.

5 53. The method of Claim 52 wherein the protective sequence is expressed in the cell.

54. The method of Claim 52 wherein the protective sequence delays and/or prevents the cell from undergoing cell death.

10

55. A method for modulating the function, activity, expression and/or level of a protective sequence in a cell comprising administering to the cell a compound which modulates the function, activity, expression and/or level of a protective sequence in the cell.

15 56. The method of Claim 55, wherein the compound inhibits the function, activity, expression and/or level of a protective sequence in the cell.

57. The method of Claim 55, wherein the compound enhances or potentiates the function, activity, expression and/or level of a protective sequence in the cell.

20

58. The methods of any one of Claims 55-57, wherein the compound is selected from the group consisting of a small organic molecule, an antibody, a ribozyme, an antisense molecule, and combinations thereof.

25 59. The method of Claim 55, wherein the protective sequence encodes a polypeptide comprising:

- (a) an amino acid sequence shown in Figures 4(A-AB);
- (b) an amino acid sequence shown in Figures 5(A-L);
- (c) an amino acid sequence shown in Figures 6(A-K);
- 30 (d) an amino acid sequence shown in Figures 7(A-Z);
- (e) an amino acid sequence shown in Figures 8(A-S);



- (f) an amino acid sequence shown in Figures 9(A-X);
- (g) an amino acid sequence shown in Figures 10(A-V);
- (h) an amino acid sequence shown in Figures 11(A-I);
- (i) an amino acid sequence shown in Figures 12(A-G); or
- (j) the amino acid sequence shown in Figure 13(A-H).

60. A primer comprising an isolated nucleic acid molecule which hybridizes under highly stringent conditions to:

- (a) a nucleic acid sequence shown in Figures 4(A-AB);
- (b) a nucleic acid sequence shown in Figures 5(A-L);
- (c) a nucleic acid sequence shown in Figures 6(A-K);
- (d) a nucleic acid sequence shown in Figures 7(A-Z);
- (e) a nucleic acid sequence shown in Figures 8(A-S);
- (f) a nucleic acid sequence shown in Figures 9(A-X);
- (g) a nucleic acid sequence shown in Figures 10(A-V);
- (h) a nucleic acid sequence shown in Figures 11(A-I);
- (i) a nucleic acid sequence shown in Figures 12(A-G);
- (j) a nucleic acid sequence shown in Figure 13 (A-H); or
- (k) a nucleic acid sequence shown in Figures 1(A-J).

61. A method for diagnosing a protective sequence-mediated condition, disorder or disease in an individual comprising obtaining a biological sample from said individual; contacting said biological sample with the primer according to claim 60; wherein if said primer interacts with said biological sample, but does not interact with a biological sample from a control individual not undergoing a protective sequence-mediated condition, disorder or disease, then a protective sequence-mediated condition, disorder or disease has been diagnosed.

62. A diagnostic kit for detecting a protective sequence-mediated condition, disorder or disease in an individual comprising a reagent in suitable packaging, wherein said reagent comprises the primer according to claim 60.

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tcgacccacg	cgtccgcgga	cgcgtgggta	ggactttgaa	gaatacagtt	tcagtggagt	60
aaactatttt	ttgtgatctg	tttacttata	ttatcctgac	tttaaacatt	ttttagcata	120
agaaaatagt	aaaaaaatat	tttaatgata	taaaatcctt	ggctgctagc	taggagtcgc	180
tctgtgctat	agtagaaaaa	tatggagact	gggagctgtg	tgatctat	tcaccagtaa	240
ctgggtgact	ttaaaaggcc	tgtaacttgt	acttgtctac	ttttatccag	ttctacactg	300
aaagattggt	tttgatgatt	ctcaacatct	ttttctggta	tgtaagactt	tcctcatgaa	360
attcagaaca	ttgccattta	aggaatggca	aagatTTTTT	ccctaaagtt	aaaagatcaa	420
atatgaaatt	aatataagtt	ataaagtata	tatttcttca	acaataatgt	acagttgaag	480
gtatgtcaaa	aattgacttt	catttataga	aaaaaaagta	aagtaggtaa	ctgtattagt	540
tctctagggg	agctgtaaca	aaataccaaa	aactgggtgg	cttaaacagc	aaaaaaatgt	600
attatctcac	agttctgcag	tctagaagtc	tggaatcaag	gtgttagtag	ggctggttct	660
ttctgagggc	tgcgaaggca	ggatatgttc	caggcctccc	tctatggctt	gtagatggcc	720
atcttcatgg	tcacatggca	ttctccctgt	agctctctgt	ttccagactt	cccctttttg	780
taaggatata	agtgatatta	gattagggtc	ttccctaagg	acctcatttg	acctgcctgg	840
gctcaagcta	ttctcccacc	tctgcctccc	taagagctgg	gattacaggc	atgagccatc	900
acacccgccc	ctcatTTTaa	tttgattacc	tctgtaaata	cctctgtctc	caaatgagat	960
ttcatcctga	gcagctgggg	gttaggactt	caatatatga	atttgacagg	gagggtagaa	1020
ggagagaaca	gaattcaacc	cacagcagca	acaatctaata	agcttcctgt	gagcaagcaa	1080
agagaatggt	cattgtcagt	ctcataggcg	ccattcccta	ttcatacgtt	acttgtgtctc	1140
tctcatattc	cttgagtgtt	ttaaattgta	aacattcaag	tacaaacaaa	cttcgcttga	1200
ttaccagaga	taaaaaagaa	atgccttgta	atttggtgtc	atgtgaatgt	tttaagtggg	1260
tacctgaaaa	attgtactta	agaatggcat	aagagctttc	tgatTTTcat	tttacttcca	1320
ttaaagggga	aaatatgcat	agactgtcta	tccattagcc	agaacaatgg	gacctctccc	1380
atcttaaaat	aaaagccaaa	ataatctggc	caccaggaag	aaagggtaga	gcttggggaat	1440
gtcctcagga	gattgtaaag	atgcgtttcc	ttgattcttt	tgctcacact	cttccctgtg	1500
actatttcct	ccttcagggc	tctatttctg	ggttgggaga	atgctgttcc	agcaccaagc	1560
agtgtgggta	tatatattca	taccaaagag	gcaatttgat	tgctccttga	gttacaaaaa	1620
accaaagtgc	aatgcctgat	tagggaatac	aacaataaaa	gtaaaaataa	tttaggagta	1680
tatatgcaga	acatcagcct	ttaaagtaata	cttttattag	gaaaatggca	ttcacgattt	1740
gagaagatgg	aagggtggtg	ggaacagaaa	taaaaaaaaa	aaaaaagggc	ggcc	1794

FIG. 1A

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tcgacccacg	cgtccgctac	ccaggaaaca	gtcccatcag	catcttagcc	tgccccactc	60
tagccacaca	taccacgtg	tactcctgag	ttcagtgtgc	ccacctcact	cccacaccct	120
cacatagact	tggcaagagt	aaggagggaa	ctccatagag	acattttacc	tatctcaggg	180
gagcagccac	aaagaagcaa	gtcttgtaaa	aggtcttttg	caaaggagag	tgaacccagc	240
aatgagagat	ccttaacagc	tagtgcccat	tagggggcta	aacctaaagc	ctgggtggtg	300
atgggtcaaa	cgctaattgag	tcagtgaatc	cttaccgacc	ccctggcctt	tataatctga	360
ggcaactttg	gctgcagccc	gggaatgtgc	agggcactag	ggaatacaag	gccttcttcc	420
ctggttggtc	tgtaataaaa	cagccatggg	gttgtccctc	cagtccgaga	gactgtgatg	480
aggcctacat	agcagcgatg	tggtcaggta	aaaatcagga	accactgaa	atcttgggca	540
agccaccctg	cctgcttggt	cctcggttct	ctcatatgtc	atatatagga	ggtgaggact	600
ccagctccac	ctgccccagg	tgggtgtggt	gatgatgagg	aaagacaaga	ggcttgcaag	660
gaccctgaag	aggtcggagc	atcatacaga	ttcctttatt	agccacatt	ctgatgttcc	720
ctggtgagac	ttgcccgaag	caattgctag	taaatggggg	ttaatttctt	ctccacctcc	780
ctactgaaca	aaaaaagaaa	aagggcggcc				810

FIG.1B

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taacagccca	atatctacaa	tcaaccaaca	agtcattatt	accctcactg	tcaacccaac	60
acaggcatgc	tcataaggaa	aggttaaaaa	aagtaaaagg	aactcggcaa	atcttacccc	120
gcctgtttac	caaaaacatc	acctctagca	tcaccagtat	tagaggcacc	gcctgcccag	180
tgacacatgt	ttaacggccg	cggtagcccta	accgtgcaaa	ggtagcataa	tcacttggtc	240
cttaattagg	gacctgtatg	aatgggtcca	cgagggttca	gctgtctctt	acttttaacc	300
agtgaattg	acctgcccgt	gaagaggcgg	gcacgacaca	gcaagacgag	aagaccctat	360
ggagctttaa	tttattaatg	caaacagtac	ctaacaaacc	cacaggtcct	aaactaccaa	420
acctgcatta	aaaatttcgg	ttggggcgac	ctcggagcag	aacccaacct	ccgagcagta	480
catgctaaga	cttcaccagt	caaagcgaac	tactatactc	aattgatcca	ataacttgac	540
caacggaaca	agttacccta	gggataacag	cgcaatccta	ttctagagtc	catatcaaca	600
atagggttta	cgacctcgat	gttggtatcag	gacatcccga	tggtgcagcc	gctatttaaag	660
gttcgtttgt	tcaacgatta	aagtcctacg	tgatctgagt	tcagaccgga	gtaatccagg	720
tcggtttcta	tctacttcaa	attcctccct	gtacgaaagg	acaagagaaa	taaggcctac	780
ttcacaaagc	gccttcccc	gtaaatgata	tcattctcaac	ttagtattat	accacacccc	840
acccaagaac	aggggtttaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	900
aaaaaaaaaa	aagggcggcc					920

FIG.1C

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tcgacccacg cgtccgcgca agatggcagc caccacgggc tcgggagtaa aagtcacctg 60
caattttccga ctgttggaag aactcgaaga aggccagaaa ggagtaggag atggcacagt 120
tagctggggt ctagaagatg acgaagacat gacacttaca agatggacag ggatgataat 180
tgggcctcca agaacaattt atgaaaaccg aatatacagc cttaaaatag aatgtggacc 240
taaataccca gaagcacccc cttttgtaag atttgtaaca aaaattaata tgaatggagt 300
aaatagttct aatggagtgg tggacccaag agccatatca gtgctagcaa aatggcagaa 360
ttcatatagc atcaaagttg tcctgcaaga gcttcggcgc ctaatgatgt ctaaagaaaa 420
tatgaaactc cctcagccgc ccgaaggaca gtgttacagc aattaatcaa aaagaaaaac 480
cacaggccct tccccttccc cccaattcga tttaatcagt cttcattttc cacagtagta 540
aattttctag atacgtcttg tagacctcaa agtaccggaa aggaagctcc cattcaaagg 600
aaatttatct taagatactg taaatgatac taattttttc gtccatttga aatatataag 660
ttgtgctata acaaatcatc ctgtcaagtg taaccactgt ccacgtagtt gaacttctgg 720
gatcaagaaa gtctatttaa attgattccc atcataactg gtggggcaca tctaactcaa 780
ctgtgaaaag acacatcaca caatcacctt gctgctgatt acacggcctg gggctctctg 840
cttctcccct taccctcccg cctcccaccc tccctgcaac aacagccctc tagcctgggg 900
ggcttgtag agtagatgtg aaggtttcag gtcgcagcct gtgggactac tgctaggtgt 960
gtggggtgtt tcgcctgcac ccctggtttc ttttaagtctt aagtgatgcc ccttccaaac 1020
catcatcctg tccccacgct cctccactcc cgcccttggc cgaagcatag attgtaaccc 1080
ctccactccc ctctgagatt ggccttcggt gaggaattca gggctttccc catatcttct 1140
ctccccacc tttatcgagg ggtgctgctt tttctccctc ctctcaagt tcctttttgc 1200
accgtcacca cccaacacct tccatgacac ttccttgctt tggccagaag ccatcaggta 1260
aggttggaag gagcctctga cctcccttgt ttagttttgg aaccatactc actcactctc 1320
caccagcctg ggaaatgaat attgggtcct cagccctgcc accctctgct gtcacagct 1380
gatgcattgt ttttagctca ggttttgata aggtgaaaag aatagtcacc agggttactc 1440
agacctgcca gctctcggag tccttggtgg ttgaacttgg agaaagaccg catgaagata 1500
cttgtaagca cacatgatcc ctctgaattg ttttactttc ctgtaactgc ttttgctttt 1560
aaaaattgaa gaagttttaa acagggtttt catttggtca tccttgcaat ccattgggggt 1620
ctagtttgga atctgacaac tggaaacaaa agaaccttga atccgggtgca tgccttggtt 1680
ttggtgctgc tgctgcttcc caagatcctc agcagggtt aagaaggaa cgggtgtgca 1740
cagcagatcc ccgaaattgg tgggcttgac ctccctggcaa attgctgcgt ctttccactt 1800
gctgttcagg accactaaat gctgaaatgt ggatgcatac cgaaataaaa gcaattcatt 1860
gtgtactaaa ggtttttttt ttttttttaa tttagtattt gtgtaaaacc accttttgaa 1920
gcagcaacta tcaagtctga aaagcaattg atgtttccat taatcttttt ctgggggggaa 1980
aaccttagtt ctaaggattt aacatcctgt aagtgaagtt taacataaca gtattccata 2040
agcagccttt ttattgtcag accattgcct gattttaata taataaaaaa aaagtgtgctg 2100
ttaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc ggcc 2144

```

FIG.1D

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```

tcgacccacg cgtccggagg caggaaaatc gcttgaaccc aggaggtgga ggttgtagtg 60
agccgagatc acaccactgc actccagcct gggtgacaag aacgaaactc catctcaaaa 120
aataaaaataa aatatatact atcttgctcc tcagaaccag tggggaagaa gagggaaggc 180
aaagaaagaa actgagcata gtaaacacag catTTTTTtg taggctctta tttaaaatgt 240
gtgtgtgtgt gtgtatgtgt gtgtttctga gtaagtattg actgggaaaa agagagaagt 300
caatcaaaaag tatactgtgc aattgagaga ggctggccca agatttaaaa cttcctgttg 360
gtaatctaac tgtgagtaga taggaatcgg ccatatgacg aaatgagatc aataggaaat 420
gtgctTTTTg aggaaatTTT atTTtagtac caaatgttgC cagtgacaat cttcagTTaa 480
gaagtaagtt atttgaccta aaattcttat ctctgccact ttggTTtaaa aacaaaaacc 540
cttatataca tggaatagtt atattTTaat taagcattta tTTtagttgt tttcatccat 600
tcaagcaaaa tgaataagca gcattTTtca ttgcacttaa aaatgtaaaa tacctgcatg 660
ccactaatct gtaacatttt accagttcag atgcctgtaa tgtgtgactt tatgtgtgtc 720
tgtgtgtgtt tgaagagaat aaaggaaata atactTTtga aactgtTTaa acaagtgttt 780
aaacttctat tggcaacatt tattgggcta agcagttatt gaaaactccg catagtTTta 840
TTTTccattt gaaacttcaa tcaaatcaag actattatat tcattagggg attaaagact 900
aatttgcttt ttaaattgtga agtggaacac tgtgtggaaa gtaaatgtgt gatgaagcaa 960
aatgtataaa gtatgaaata ttatactTTT accctggata attattcagg accccagttg 1020
gcccaaatag gtgcaatttt taatcctttg aaattagcca gccagaccta atgctaaggt 1080
aaatgtaaac tgTTTTaatt aattaagatc tttctgcttt cgaaggtata atgtatctat 1140
ttctgtcagg aatgatattt ccaaatgaaa atgtaaagaa cattgggaaa taataaactt 1200
tcctttcaaa gtaaaaagtaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1260
aaaaaaaaaa aaaaaaaaaa aaaaagggcg gcc 1293

```

FIG. 1E

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tcgacccacg	cgtccggttg	ttaaacccta	tgaagagtaa	cagtgtagac	cagactgcct	60
ctctcagata	tgtgcctgat	atthttgtgga	tacctcccct	gcactggcaa	aacactatgc	120
ttttgggtgt	tagactgaaa	tattttaaga	gtatttaacc	tttccagtat	tctgtttcac	180
gcttagatgg	aaatgtatct	tatgaataga	gacatattaa	aataatgttt	acatcttaga	240
aaaaacatag	atagtgtctag	taatattact	tataactgta	atatatagat	tcagaaatac	300
atthttcatta	tccaaaatca	gcttcaacaa	atggthttctg	gagacaaata	atthgtthttc	360
attatcattg	tataatcagg	ttaatgattt	atthttttgac	taaatgtgca	atthcttattc	420
actagataac	thttcagtatc	agtgggtggtt	acttattact	taaatcagag	gaaggatttt	480
ataaagatta	ataaatttaa	thttaccaat	aaatattccc	ataatttaga	aaaggatgtc	540
gacttgctaa	thttcagaaat	aattattcat	thtttaaaaag	cccctthtaa	agcatctact	600
tgaagattgg	tataatthttc	ataaaatgtc	thttthtttta	gtgtcccaaa	gatatcttag	660
ataaactatt	ttgaagtcca	gatttcagat	gaggcaacat	thttcttgaga	taattaccca	720
agthttcatcc	atgttgaaatg	gtacaaaata	thttctgtgaa	actaacagga	agatathtttc	780
agataactag	gataacttgt	tgctthtgta	cccagcctaa	ttgaagagtg	gcagagacta	840
ctacaaaaag	caacctthttc	atthttcacta	agagthttaaa	agctattgta	ttattaaaaa	900
gtctthtaca	tgcttgthttc	aaagaaccaa	cagaaaaaaa	agctaagaaa	actgagaact	960
aacattaaaa	aaattaaatt	tagaataaga	atgattthctt	taatttgctc	thttthttctt	1020
tggtctaaaa	cattattaaa	thtttgtaaa	tattthtgatt	taatgtgtct	tagatcctca	1080
ttattthta	acaggaaaag	aaaagattta	gtaattthctt	accatgctaa	tatgtaaagt	1140
tcatgccatc	caggcattta	agagcgatcc	tcatcccttc	agcaatatgt	atthtgagttc	1200
acactathttc	tgthtttacag	cagthtttgaa	aaacacatac	tatgccacca	atthgtcatat	1260
tattthttaga	tgatgtaaca	tagccatcaa	aattaatatt	atgtaatgcc	taatacttag	1320
tatgtaaatg	tcacgagatc	atthtttacat	taaacgtgaa	aaaaaatcaa	aaaaaaaaaa	1380
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1440
aaaaaaaaaa	aaaaaaaaag	gcggcc				1466

FIG. 1F

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tcgacccacg	cgtccgcca	cgcgtccgca	agagcatctt	cagcgggcga	gtccccggct	60
cctccagctc	cttcctctc	ttcctctcc	tcctccacct	ccggcttttg	ggggatcact	120
gtcctctctc	ggcagcagaa	tgagccggca	ggtggtccgc	tccagcaagt	tccgccacgt	180
gtttggacag	ccggccaagg	ccgaccagt	ctatgaagat	gtgcgcgtct	cacagaccac	240
ctgggacagt	ggcttctgtg	ctgtcaaccc	taagtttgtg	gccctgatct	gtgaggccag	300
cgggggaggg	gccttcctgg	tgctgcccct	gggcaagact	ggacgtgtgg	acaagaatgc	360
gcccacggtc	tgtggccaca	cagcccctgt	gctagacatc	gcctggtgcc	cgcacaatga	420
caacgtcatt	gccagtggct	ccgaggactg	cacagtcatg	gtgtgggaga	tcccagatgg	480
gggcctgatg	ctgcccctgc	gggagcccgt	cgtaaccctg	gagggccaca	ccaagcgtgt	540
gggcattgtg	gcctggcaca	ccacagccca	gaacgtgctg	ctcagtgcag	gttgtgacaa	600
cgtgatcatg	gtgtgggacg	tgggcactgg	ggcggccatg	ctgacactgg	gcccagaggt	660
gcacccagac	acgatctaca	gtgtggactg	gagccgagat	ggaggcctca	tttgtacctc	720
ctgccgtgac	aagcgcgtgc	gcatcatcga	gccccgaaa	ggcactgtcg	tagctgagaa	780
ggaccgtccc	cacgagggga	cccggcccgt	gcgtgcagt	ttcgtgtcgg	aggggaagat	840
cctgaccacg	ggcttcagcc	gcatgagtga	gcggcagggt	gcgctgtggg	acacaaagca	900
cctggaggag	ccgctgtccc	tgcaggagct	ggacaccagc	agcgggtgtc	tgctgccctt	960
ctttgacctt	gacaccaaca	tcgtctacct	ctgtggcaag	ggtgacagct	caatccggta	1020
ctttgagatc	acttccgagg	cccctttcct	gcactatctc	tccatgttca	gttccaagga	1080
gtcccagcgg	ggcatgggct	acatgcccaa	acgtggcctg	gaggtgaaca	agtgtgagat	1140
cgccaggttc	tacaagctgc	acgagcggag	gtgtgagccc	attgccatga	cagtgcctcg	1200
aaagtcggac	ctgttccagg	aggacctgta	cccacccacc	gcagggcccg	accctgccct	1260
cacggctgag	gagtggctgg	ggggtcggga	tgctgggccc	ctcctcatct	ccctcaagga	1320
tggctacgta	cccccaaaga	gccgggagct	gagggtaaac	cggggcctgg	acaccgggcg	1380
caggagggca	gcaccagagg	ccagtggcac	tcccagctcg	gatgccgtgt	ctcggctgga	1440
ggaggagatg	cggaagctcc	aggccacggt	gcaggagctc	cagaagcgct	tggacaggct	1500
ggaggagaca	gtccaggcca	agtagagccc	cgcagggcct	ccagcagggt	cagccattca	1560
cacccatcca	ctcacctccc	attcccagcc	acatggcaga	gaaaaaaatc	ataataaaat	1620
ggctttat	tctggtaaaa	aaaaaaaaaa	agggcggcc			1659

FIG. 1 G



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tcgacccacg	cgtccgctct	gccgcagcct	gtgccgccgc	cgcctcctgg	gaagagagga	60
agcgggagag	gagcccacgt	ctcctgtcac	ccaatatctc	cagccgcgca	gtcccgaaga	120
gtgtaagatg	ttcgcctgcg	ccaagctcgc	ctgcaccccc	tctctgatcc	gagctggatc	180
cagagttgca	tacagaccaa	tttctgcatc	agtgttatct	cgaccagagg	ctagtaggac	240
tggagagggc	tctacgggat	ttaatggggc	ccagaatggg	gtgtctcagc	taatccaaag	300
ggagtttcag	accagtgcaa	tcagcagaga	cattgatact	gctgccaaat	ttattgggtgc	360
aggtgctgca	acagtaggag	tggctggttc	tgggtgctgg	attggaacag	tctttggcag	420
ccttatcatt	ggttatgcca	gaaacccttc	gctgaagcag	cagctgttct	catatgctat	480
cctgggattt	gccttgtctg	aagctatggg	tctcttttgt	ttgatggttg	ctttcttgat	540
tttgtttgcc	atgtaacaaa	ttactgcttg	acatgttggc	attcatatta	attacggatg	600
taattctgtg	tatcttactg	tgactccgaa	aactgtagta	ttgggtgcat	gggaatgtac	660
gttatttcca	aagtcatttc	attaaagatg	aaaactttta	aaaaaaaaaa	aaaagggcgg	720
cc						722

FIG. 1H

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```
tcgacccacg cgtccggatt tagcaggaag ctgtgagagc agtttggttt ctagcatgaa 60
gacagagccc caccctcaga tgcacatgag ctggcgggat tgaaggatgc tgtcttcgta 120
ctgggaaagg gattttcagc cctcagaatc gctccacctt gcagctctcc ccttctctgt 180
attcctagaa actgacacat gctgaacatc acagcttatt tcctcatttt tataatgtcc 240
cttcacaaac ccagtgtttt aggagcatga gtgccgtgtg tgtgcgtcct gtcggagccc 300
tgtctctctt ctctgtaata aactcatttc tagcagaaaa aaaaaaaaaa aaaaaagggc 360
ggcc
```

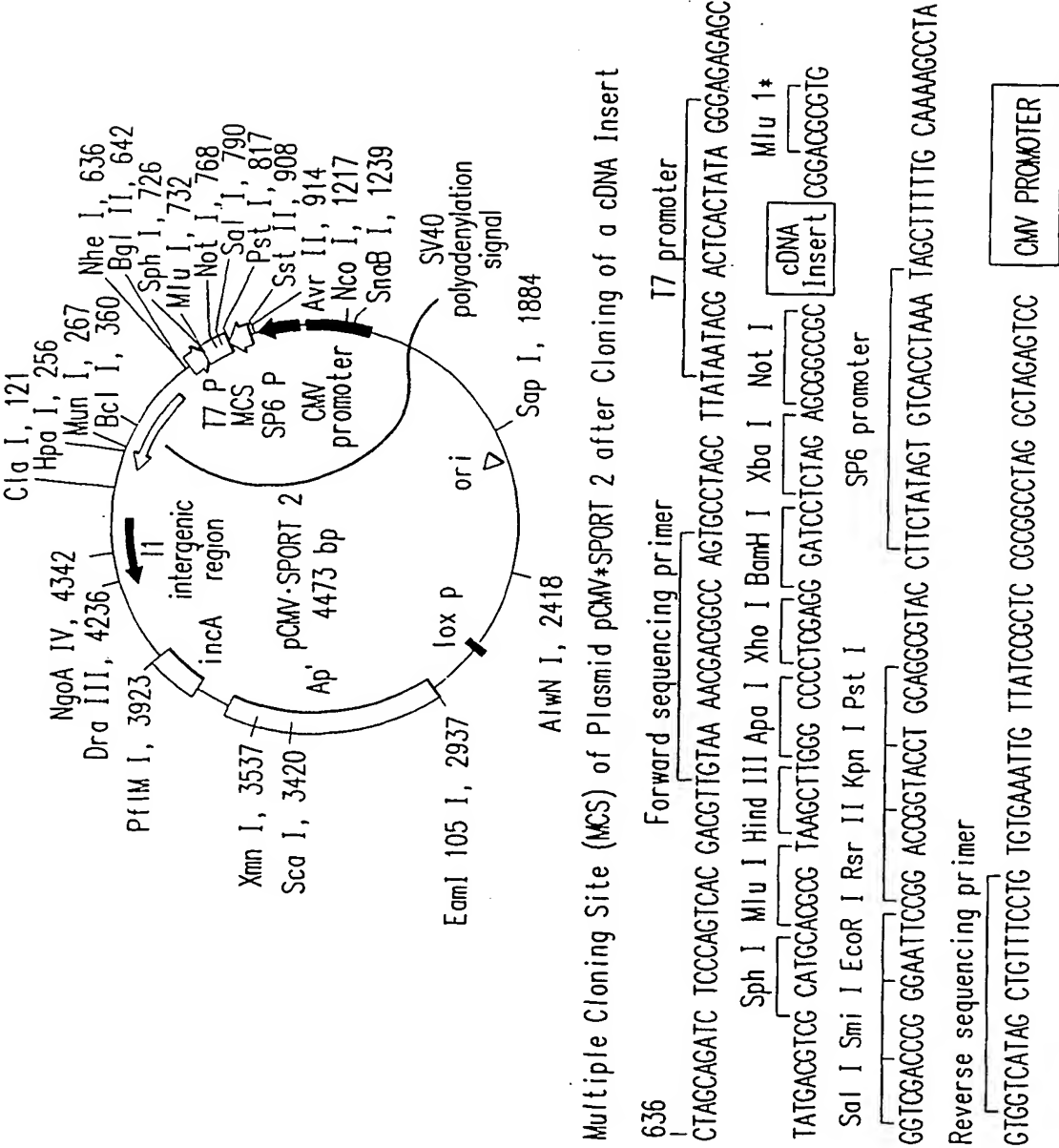
FIG. 11

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tccgctctta	gtaagattac	acatgcaagc	atccccgttc	cagtgagttc	accctctaaa	60
tcaccacgat	caaaagggac	aagcatcaag	cacgcagcaa	tgcagctcaa	aacgcttagc	120
ctagccacac	ccccacggga	aacagcagtg	attaaccttt	agcaataaac	gaaagtttaa	180
ctaagctata	ctaaccacag	ggttgggtcaa	tttcgtgcc	gccaccgcgg	tcacacgatt	240
aacccaagtc	aatagaagcc	ggcgtaaaga	gtgttttaga	tcaccccctc	cccaataaag	300
ctaaaactca	cctgagttgt	aaaaaactcc	agttgacaca	aaatagacta	cgaaagtggc	360
tttaacatat	ctgaacacac	aatagctaag	acccaaactg	ggattagata	ccccactatg	420
cttagcccta	aacctcaaca	gttaaataca	caaaactgct	cgccagaaca	ctacgagcca	480
cagcttaaaa	ctcaaaggac	ctggcggtgc	ttcatacccc	tctagaggag	cctgttctgt	540
aatcgataaa	ccccgatcaa	cctcaccacc	tcttgctcag	cctatatatacc	gccatcttca	600
gcaaaccctg	atgaaggcta	caaagtaagc	gcaagtacc	acgtaaagac	gttaggtcaa	660
ggtgtagccc	atgggggtgg	aagaaatggg	ctacattttc	taccccagaa	aactacgata	720
gcccttatga	aacttaaggg	tcgaagggtg	atttagcagt	aaactgagag	tagagtgtt	780
agttgaacag	ggccctgaag	cgcgtagaca	ccgcccgtca	ccctcctcaa	gtatacttca	840
aaggacattt	aactaaaacc	cctacgcatt	tatatagagg	agacaagtcg	taacatggta	900
agtgtactgg	aaagtgcact	tggacgaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	960
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1020
aaaaaaaaaa	aaaaaaaagg	gcggcc				1046

FIG. 1J

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\*This Mlu I restriction site contained within the Sal I adapter is introduced into the pCMV\*SPORT 2 vector upon ligation of the cDNA insert. Due to flanking sites, Mlu I, by itself, or the combined Not I-Sal I digestion can be used to completely excise the cDNA insert.

FIG. 2

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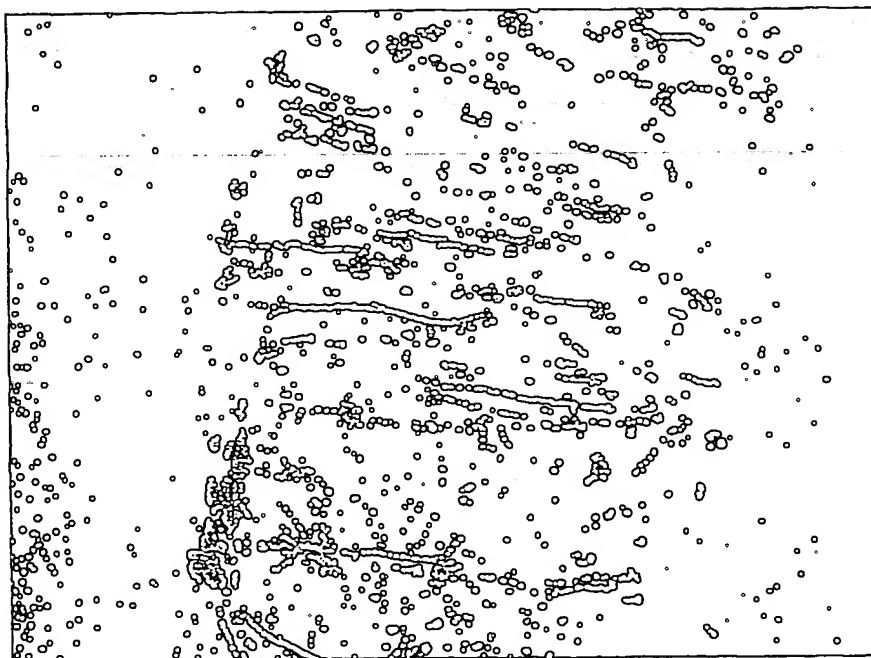


FIG. 3A

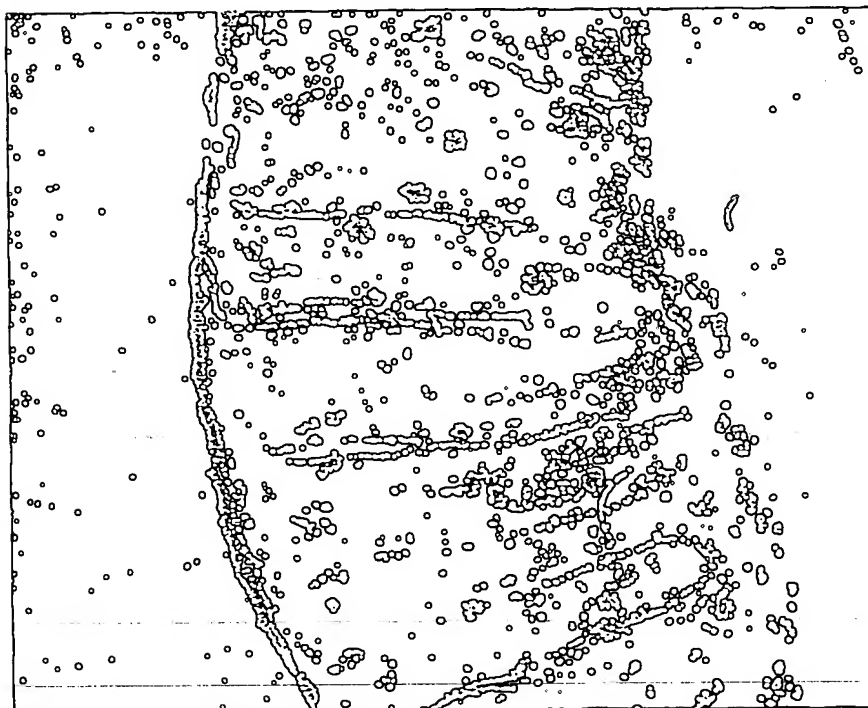


FIG. 3B

SUBSTITUTE SHEET (RULE 26)

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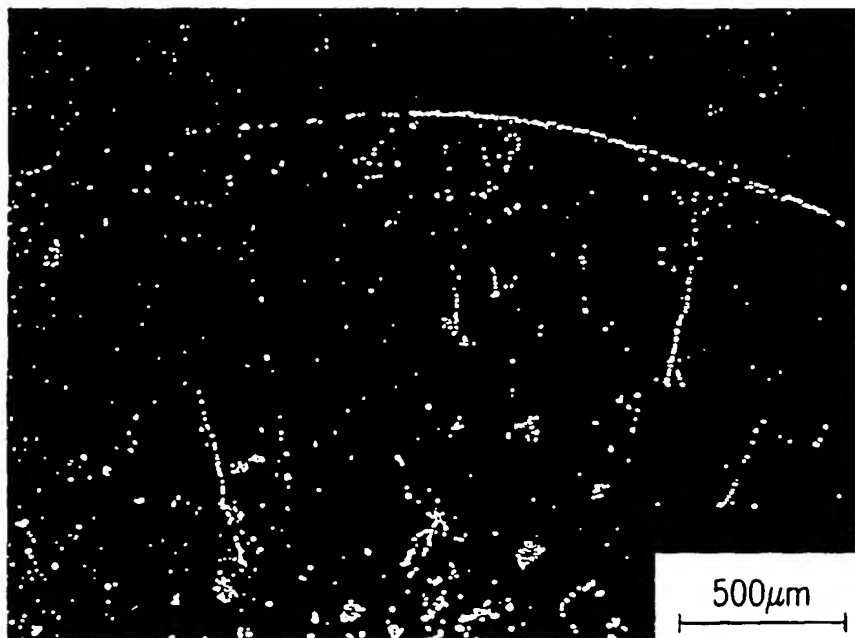


FIG.3C

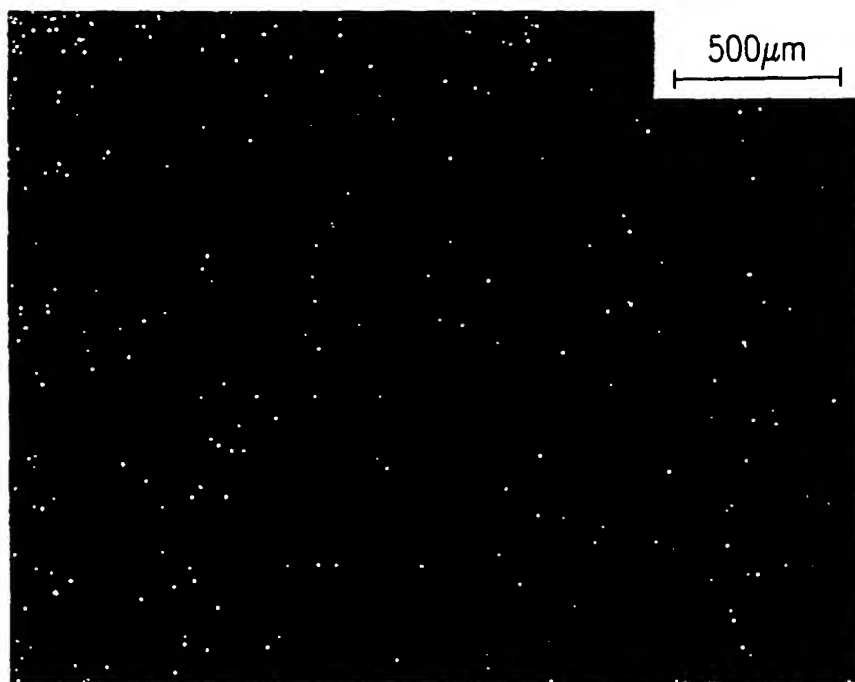


FIG.3D

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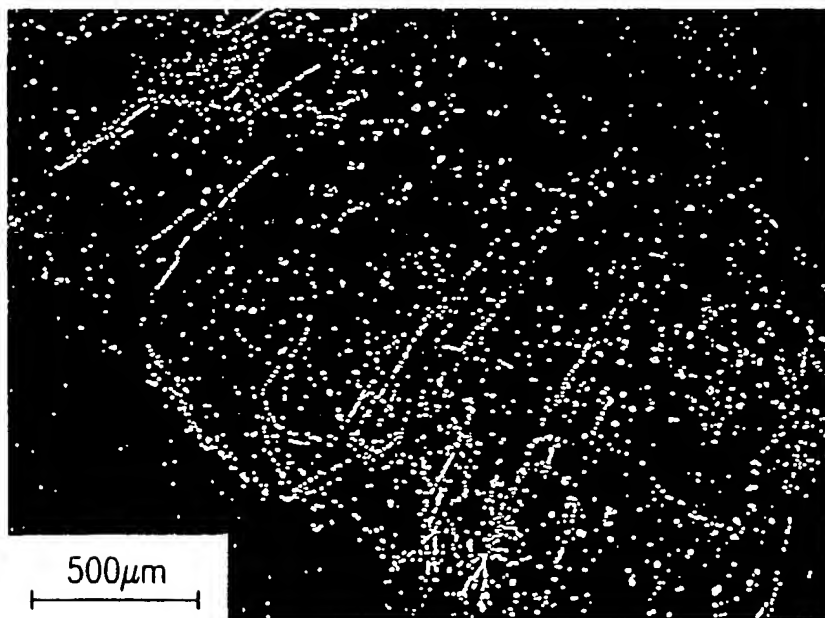


FIG.3E

COMPARISON OF NEURONAL PROTECTION IN STROKED RAT CORTICAL  
BRAIN SLICES

SEQUENCE DESIGNATION	AVERAGE SURVIVING NEURONS PER SLICE (n) @ 3 DAYS POST-STROKE
EGFP CONTROL (NEGATIVE CONTROL)	1.01 (41)
CNI-00718	20.6 (6)
CNI-00722	21 (6)
CNI-00725	14.3 (9)
CNI-00726	19.7 (3)
CNI-00727	17.8 (9)
CNI-00728	10.7 (3)
CNI-00729	13 (3)
CNI-00730	14.7 (3)
CNI-00731	11.7 (3)
CNI-00732	12.7 (3)

FIG. 3F



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atggagactg ggagctgtgt gatctatattt caccagtaa 39

Met	Glu	Thr	Gly	Ser	Cys	Val	Ile	Tyr	Phe	His	Gln
1				5					10		

FIG.4A

atgattctca acatcttttt ctggtatgta agactttcct catga 45

Met	Ile	Leu	Asn	Ile	Phe	Phe	Trp	Tyr	Val	Arg	Leu	Ser	Ser
1				5					10				

FIG.4B

atgaaattca gaacattgcc atttaaggaa tggcaaagat tttttcccta a 51

Met	Lys	Phe	Arg	Thr	Leu	Pro	Phe	Lys	Glu	Trp	Gln	Arg	Phe	Phe	Pro
1				5				10					15		

FIG.4C

atggcaaaga ttttttcctt aaagttaaaa gatcaaatat ga 42

Met	Ala	Lys	Ile	Phe	Ser	Leu	Lys	Leu	Lys	Asp	Gln	Ile
1				5				10				

FIG.4D

atgaaattaa tataa 15

Met	Lys	Leu	Ile
1			

FIG.4E

atgtacagtt ga 12

Met	Tyr	Ser
1		

FIG.4F

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atgtcaaaaa ttgactttca tttatag 27

Met Ser Lys Ile Asp Phe His Leu

1

5

FIG.4G

atgtattatc tcacagttct gcagtctaga agtctggaat caaggtgtta g 51

Met Tyr Tyr Leu Thr Val Leu Gln Ser Arg Ser Leu Glu Ser Arg Cys

1

5

10

15

FIG.4H

atgttccagg cctccctcta tggcttgtag 30

Met Phe Gln Ala Ser Leu Tyr Gly Leu

1

5

FIG.4I

atggcttgta gatggccatc ttcattgtca catggcattc tccctgtagc tctctgtttc 60  
 cagacttccc ctttttgtaa ggatatcagt gatattagat tagggctctc cctaaggacc 120  
 catttgacct gcctgggctc aagctattct cccacctctg cctccctaag agctggggatt 180  
 acaggcatga gccatcacac ccgcccctca ttttaatttg a 221

Met Ala Cys Arg Trp Pro Ser Ser Trp Ser His Gly Ile Leu Pro Val  
 1 5 10 15

Ala Leu Cys Phe Gln Thr Ser Pro Phe Cys Lys Asp Ile Ser Asp Ile  
 20 25 30

Arg Leu Gly Ser Ser Leu Arg Thr Ser Phe Asp Leu Pro Gly Leu Lys  
 35 40 45

Leu Phe Ser His Leu Cys Leu Pro Lys Ser Trp Asp Tyr Arg His Glu  
 50 55 60

Pro Ser His Pro Pro Leu Ile Leu Ile  
 65 70

FIG.4J

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atggccatct tcatgggtcac atggcattct ccctgtagct ctctgtttcc agacttcccc 60  
 tttttgtaa 69

Met Ala Ile Phe Met Val Thr Trp His Ser Pro Cys Ser Ser Leu Phe  
 1 5 10 15  
 Pro Asp Phe Pro Phe Leu  
 20

FIG.4K

atggtcacat ggcattctcc ctgtagctct ctgtttccag acttccccctt ttgttaa 57  
 Met Val Thr Trp His Ser Pro Cys Ser Ser Leu Phe Pro Asp Phe Pro  
 1 5 10 15  
 Phe Leu

FIG.4L

atggcattct ccctgtag 18

Met Ala Phe Ser Leu  
 1 5

FIG.4M

atgagccatc acaccgccc ctcatttttaa 30

Met Ser His His Thr Arg Pro Ser Phe  
 1 5

FIG.4N

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```

atgagatttc atcctgagca gctgggggtt aggacttcaa tatatgaatt tgacagggag 60
ggtagaagga gagaacagaa ttcaaccac agcagcaaca atctaatagc ttcctgtgag 120
caagcaaaga gaatgttcat tgtcagtctc ataggcgcca ttcctattc atacgttact 180
tgtgtctctt catattcctt gagtgtttta aattgtaaac attcaagtac aaacaaactt 240
cgcttgatta ccagagataa aaaagaaatg ccttgtaatt tgggtgtcatg tgaatgtttt 300
aagtggatac ctgaaaaatt gtacttaaga atggcataa 339

```

```

Met Arg Phe His Pro Glu Gln Leu Gly Val Arg Thr Ser Ile Tyr Glu
 1           5           10           15
Phe Asp Arg Glu Gly Arg Arg Arg Glu Gln Asn Ser Thr His Ser Ser
          20           25           30
Asn Asn Leu Ile Ala Ser Cys Glu Gln Ala Lys Arg Met Phe Ile Val
          35           40           45
Ser Leu Ile Gly Ala Ile Pro Tyr Ser Tyr Val Thr Cys Ala Leu Ser
          50           55           60
Tyr Ser Leu Ser Val Leu Asn Cys Lys His Ser Ser Thr Asn Lys Leu
65           70           75           80
Arg Leu Ile Thr Arg Asp Lys Lys Glu Met Pro Cys Asn Leu Val Ser
          85           90           95
Cys Glu Cys Phe Lys Trp Ile Pro Glu Lys Leu Tyr Leu Arg Met Ala
          100          105          110

```

## FIG.4O

```

atgaatttga cagggagggt agaaggagag aacagaattc aaccacagc agcaacaatc 60
taa 63

```

```

Met Asn Leu Thr Gly Arg Val Glu Gly Glu Asn Arg Ile Gln Pro Thr
 1           5           10           15
Ala Ala Thr Ile
          20

```

## FIG.4P

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atgttcattg tcagtctcat aggcgccatt ccttattcat acgttacttg tgctctctca 60  
 tattccttga gtgttttaaa ttgtaaacat tcaagtacaa acaaacttcg cttgattacc 120  
 agagataaaa aagaaatgcc ttgtaatttg gtgtcatgtg aatgttttaa gtggatacct 180  
 gaaaaattgt acttaagaat ggcataa 207

Met Phe Ile Val Ser Leu Ile Gly Ala Ile Pro Tyr Ser Tyr Val Thr  
 1 5 10 15  
 Cys Ala Leu Ser Tyr Ser Leu Ser Val Leu Asn Cys Lys His Ser Ser  
 20 25 30  
 Thr Asn Lys Leu Arg Leu Ile Thr Arg Asp Lys Lys Glu Met Pro Cys  
 35 40 45  
 Asn Leu Val Ser Cys Glu Cys Phe Lys Trp Ile Pro Glu Lys Leu Tyr  
 50 55 60  
 Leu Arg Met Ala  
 65

FIG.4Q

atgccttgta atttggtgtc atgtgaatgt ttaagtga tacctgaaaa attgtactta 60  
 agaatggcat aa 72

Met Pro Cys Asn Leu Val Ser Cys Glu Cys Phe Lys Trp Ile Pro Glu  
 1 5 10 15  
 Lys Leu Tyr Leu Arg Met Ala  
 20

FIG.4R

atgcatagac tgtctatcca ttag 24

Met His Arg Leu Ser Ile His  
 1 5

FIG.4S

atgggacctc tcccatctta a 21

Met Gly Pro Leu Pro Ser  
 1 5

FIG.4T

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atgtcctcag gagattgtaa agatgcgttt ccttga 36

Met Ser Ser Gly Asp Cys Lys Asp Ala Phe Pro  
 1 5 10

## FIG.4U

atgcgtttcc ttgattcttt tgctcacact cttccctgtg actatttcct ccttcagggc 60  
 tctattttctg ggttgggaga atgctgttcc agcaccaagc agtgtgggta tatatattca 120  
 taccaaagag gcaatttgat tgtccttgga gttacaaaaa accaaatgtc aatgcctgat 180  
 tag 183

Met Arg Phe Leu Asp Ser Phe Ala His Thr Leu Pro Cys Asp Tyr Phe  
 1 5 10 15  
 Leu Leu Gln Gly Ser Ile Ser Gly Leu Gly Glu Cys Cys Ser Ser Thr  
 20 25 30  
 Lys Gln Cys Gly Tyr Ile Tyr Ser Tyr Gln Arg Gly Asn Leu Ile Val  
 35 40 45  
 Leu Gly Val Thr Lys Asn Gln Met Ser Met Pro Asp  
 50 55 60

## FIG.4V

atgctgttcc agcaccaagc agtgtgggta tatatattca taccaaagag gcaatttgat 60  
 tgtccttgga gttacaaaaa accaaatgtc aatgcctga 99

Met Leu Phe Gln His Gln Ala Val Trp Val Tyr Ile Phe Ile Pro Lys  
 1 5 10 15  
 Arg Gln Phe Asp Cys Pro Trp Ser Tyr Lys Lys Pro Asn Val Asn Ala  
 20 25 30

## FIG.4W

atgtcaatgc ctgattag 18

Met Ser Met Pro Asp  
 1 5

## FIG.4X

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atgcctgatt ag 12

Met Pro Asp

1

FIG.4Y

atgcagaaca tcagccttta a 21

Met Gln Asn Ile Ser Leu

1

5

FIG.4Z

atggcattca cgatttga 18

Met Ala Phe Thr Ile

1

5

FIG.4AA

atggaaggtg gtggggaaca gaaataa 27

Met Glu Gly Gly Gly Glu Gln Lys

1

5

FIG.4AB

23/66

atgagagatc cttaa 15

Met Arg Asp Pro

1

FIG.5A

atggctcaaa cgctaatgag tcagtga 27

Met Ala Gln Thr Leu Met Ser Gln

1

5

FIG.5B

atgagtcagt ga 12

Met Ser Gln

1

FIG.5C

atgtgcaggg cactagggaa tacaaggcct tcttccttg ttgtcttgta a 51

Met Cys Arg Ala Leu Gly Asn Thr Arg Pro Ser Ser Leu Val Val Leu

1

5

10

15

FIG.5D

atggggttgt ccctccagtc cgagagactg tga 33

Met Gly Leu Ser Leu Gln Ser Glu Arg Leu

1

5

10

FIG.5E

atgaggccta catag 15

Met Arg Pro Thr

1

FIG.5F



24/66

atgtggtcag gtaaaaatca ggaaccact gaaatcttgg gcaagccacc ctgcctgctt 60  
 gtgcctcggg tcttcatat gtcatatata ggaggtgagg actccagctc cacctgcccc 120  
 aggtgggtgt ggtga 135

Met Trp Ser Gly Lys Asn Gln Glu Pro Thr Glu Ile Leu Gly Lys Pro  
 1 5 10 15  
 Pro Cys Leu Leu Val Pro Arg Phe Ser His Met Ser Tyr Ile Gly Gly  
 20 25 30  
 Glu Asp Ser Ser Ser Thr Cys Pro Arg Trp Val Trp  
 35 40

FIG.5G

atgtcatata taggaggtga ggactccagc tccacctgcc ccaggtgggt gtggtga 57

Met Ser Tyr Ile Gly Gly Glu Asp Ser Ser Ser Thr Cys Pro Arg Trp  
 1 5 10 15  
 Val Trp

FIG.5H

atgatgagga aagacaagag gcttgcaagg accctgaaga ggtcggagca tcatacagat 60  
 tcctttatta gcccacattc tgatgttccc tgggtga 96

Met Met Arg Lys Asp Lys Arg Leu Ala Arg Thr Leu Lys Arg Ser Glu  
 1 5 10 15  
 His His Thr Asp Ser Phe Ile Ser Pro His Ser Asp Val Pro Trp  
 20 25 30

FIG.5I

atgaggaaag acaagaggct tgcaaggacc ctgaagaggt cggagcatca tacagattcc 60  
 tttattagcc cacattctga tgttccttg tga 93

Met Arg Lys Asp Lys Arg Leu Ala Arg Thr Leu Lys Arg Ser Glu His  
 1 5 10 15  
 His Thr Asp Ser Phe Ile Ser Pro His Ser Asp Val Pro Trp  
 20 25 30

FIG.5J

25/66

atgttcctg gtgagacttg cccaagcaa ttgctagtaa atgggggtta a . 51

Met	Phe	Pro	Gly	Glu	Thr	Cys	Pro	Lys	Gln	Leu	Leu	Val	Asn	Gly	Gly
1				5				10						15	

FIG.5K

atgggggtta atttcttctc cacctcccta ctgaacaaaa aaagaaaaag ggcggcc 57

Met	Gly	Val	Asn	Phe	Phe	Ser	Thr	Ser	Leu	Leu	Asn	Lys	Lys	Arg	Lys
1				5				10						15	

Arg Ala Ala

FIG.5L

26/66

atgctcataa ggaaaggta a 21

Met Leu Ile Arg Lys Gly  
 1 5

FIG.6A

atgtttaacg gccgcggtac cctaaccgtg caaaggtag 39

Met Phe Asn Gly Arg Gly Thr Leu Thr Val Gln Arg  
 1 5 10

FIG.6B

atgaatggct ccacgagggt tcagctgtct cttactttta accagtga 48

Met Asn Gly Ser Thr Arg Val Gln Leu Ser Leu Thr Phe Asn Gln  
 1 5 10 15

FIG.6C

atggctccac gagggttcag ctgtctctta cttttaacca gtgaaattga cctgcccgtg 60  
 aagaggcggg catga 75

Met Ala Pro Arg Gly Phe Ser Cys Leu Leu Leu Leu Thr Ser Glu Ile  
 1 5 10 15  
 Asp Leu Pro Val Lys Arg Arg Ala  
 20

FIG.6D

atgacacagc aagacgagaa gaccctatgg agctttaatt tattaatgca aacagtacct 60  
 aacaaacca caggtcctaa actaccaaac ctgcattaa 99

Met Thr Gln Gln Asp Glu Lys Thr Leu Trp Ser Phe Asn Leu Leu Met  
 1 5 10 15  
 Gln Thr Val Pro Asn Lys Pro Thr Gly Pro Lys Leu Pro Asn Leu His  
 20 25 30

FIG.6E

atggagcttt aa 12

Met Glu Leu  
 1

FIG.6F

SUBSTITUTE SHEET (RULE 26)

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atgcaaacag tacctaacaa acccacaggt cctaaactac caaacctgca ttaa 54

Met	Gln	Thr	Val	Pro	Asn	Lys	Pro	Thr	Gly	Pro	Lys	Leu	Pro	Asn	Leu
1				5					10					15	
His															

FIG.6G

atgctaagac ttcaccagtc aaagcgaact actataactca attga 45

Met	Leu	Arg	Leu	His	Gln	Ser	Lys	Arg	Thr	Thr	Ile	Leu	Asn
1				5					10				

FIG.6H

atgttggatc	aggacatccc	gatggtgcag	ccgctattaa	aggttcgttt	gttcaacgat	60
taa						63

Met	Leu	Asp	Gln	Asp	Ile	Pro	Met	Val	Gln	Pro	Leu	Leu	Lys	Val	Arg
1				5					10					15	
Leu	Phe	Asn	Asp												
				20											

FIG.6I

atggtgcagc cgctattaaa gggtcgtttg ttcaacgatt aa 42

Met	Val	Gln	Pro	Leu	Leu	Lys	Val	Arg	Leu	Phe	Asn	Asp
1				5					10			

FIG.6J

atgatatcat	ctcaacttag	tattataccc	acaccacccc	aagaacaggg	tttaaaaaaa	60
aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaagg	gcggcc	116

Met	Ile	Ser	Ser	Gln	Leu	Ser	Ile	Ile	Pro	Thr	Pro	Thr	Gln	Glu	Gln
1				5					10					15	
Gly	Leu	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys
				20				25					30		
Lys	Lys	Lys	Lys	Gly	Arg										
				35											

FIG.6K

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```

atggcagcca ccacgggctc gggagtaaaa gtccctcgca atttccgact gttggaagaa   60
ctcgaagaag gccagaaagg agtaggagat ggcacagtta gctgggggtct agaagatgac   120
gaagacatga cacttacaag atggacaggg atgataattg ggcctccaag aacaatttat   180
gaaaaccgaa tatacagcct taaaatagaa tgtggaccta aataccaga agcaccccc   240
tttgtaagat ttgtaacaaa aattaatatg aatggagtaa atagttctaa tggagtggtg   300
gaccaagag ccatatcagt gctagcaaaa tggcagaatt catatagcat caaagttgtc   360
ctgcaagagc ttcggcgctt aatgatgtct aaagaaaata tgaaactccc tcagccgccc   420
gaaggacagt gttacagcaa ttaa                                           444

```

```

Met Ala Ala Thr Thr Gly Ser Gly Val Lys Val Pro Arg Asn Phe Arg
 1           5           10           15
Leu Leu Glu Glu Leu Glu Glu Gly Gln Lys Gly Val Gly Asp Gly Thr
      20           25           30
Val Ser Trp Gly Leu Glu Asp Asp Glu Asp Met Thr Leu Thr Arg Trp
      35           40           45
Thr Gly Met Ile Ile Gly Pro Pro Arg Thr Ile Tyr Glu Asn Arg Ile
      50           55           60
Tyr Ser Leu Lys Ile Glu Cys Gly Pro Lys Tyr Pro Glu Ala Pro Pro
65           70           75           80
Phe Val Arg Phe Val Thr Lys Ile Asn Met Asn Gly Val Asn Ser Ser
      85           90           95
Asn Gly Val Val Asp Pro Arg Ala Ile Ser Val Leu Ala Lys Trp Gln
      100          105          110
Asn Ser Tyr Ser Ile Lys Val Val Leu Gln Glu Leu Arg Arg Leu Met
      115          120          125
Met Ser Lys Glu Asn Met Lys Leu Pro Gln Pro Pro Glu Gly Gln Cys
      130          135          140
Tyr Ser Asn
145

```

FIG.7A

```

atggcacagt tagctgggggt ctag   24

```

```

Met Ala Gln Leu Ala Gly Val
 1           5

```

FIG.7B

```

atgacgaaga catga   15

```

```

Met Thr Lys Thr
 1

```

FIG.7C

SUBSTITUTE SHEET (RULE 26)

29/66

```

atgacactta caagatggac agggatgata attgggcctc caagaacaat ttatgaaaac 60
cgaatataca gccttaaaat agaatgtgga cctaaatacc cagaagcacc cccctttgta 120
agatttgtaa caaaaattaa tatgaatgga gtaaatagtt ctaatggagt ggtggaccca 180
agagccatat cagtgctagc aaaatggcag aattcatata gcatcaaagt tgtcctgcaa 240
gagcttcggc gcctaataat gtctaaagaa aatatgaaac tccctcagcc gcccgaggga 300
cagtgttaca gcaattaa                                     318

```

```

Met Thr Leu Thr Arg Trp Thr Gly Met Ile Ile Gly Pro Pro Arg Thr
 1           5           10           15
Ile Tyr Glu Asn Arg Ile Tyr Ser Leu Lys Ile Glu Cys Gly Pro Lys
          20           25           30
Tyr Pro Glu Ala Pro Pro Phe Val Arg Phe Val Thr Lys Ile Asn Met
          35           40           45
Asn Gly Val Asn Ser Ser Asn Gly Val Val Asp Pro Arg Ala Ile Ser
          50           55           60
Val Leu Ala Lys Trp Gln Asn Ser Tyr Ser Ile Lys Val Val Leu Gln
65           70           75           80
Glu Leu Arg Arg Leu Met Met Ser Lys Glu Asn Met Lys Leu Pro Gln
          85           90           95
Pro Pro Glu Gly Gln Cys Tyr Ser Asn
          100          105

```

FIG.7D

```

atggacaggg atgataattg ggcctccaag aacaatttat ga 42

```

```

Met Asp Arg Asp Asp Asn Trp Ala Ser Lys Asn Asn Leu
 1           5           10

```

FIG.7E

30/66

atgataattg ggcctccaag aacaatttat gaaaaccgaa tatacagcct taaaatagaa 60  
 tgtggaccta aataccaga agcaccaccc tttgtaagat ttgtaacaaa aattaatatg 120  
 aatggagtaa atagttctaa tggagtgggtg gacccaagag ccatatcagt gctagcaaaa 180  
 tggcagaatt catatagcat caaagtgtgc ctgcaagagc ttcggcgccct aatgatgtct 240  
 aaagaaaata tgaaactccc tcagccgccc gaaggacagt gttacagcaa ttaa 294

Met Ile Ile Gly Pro Pro Arg Thr Ile Tyr Glu Asn Arg Ile Tyr Ser  
 1 5 10 15  
 Leu Lys Ile Glu Cys Gly Pro Lys Tyr Pro Glu Ala Pro Pro Phe Val  
 20 25 30  
 Arg Phe Val Thr Lys Ile Asn Met Asn Gly Val Asn Ser Ser Asn Gly  
 35 40 45  
 Val Val Asp Pro Arg Ala Ile Ser Val Leu Ala Lys Trp Gln Asn Ser  
 50 55 60  
 Tyr Ser Ile Lys Val Val Leu Gln Glu Leu Arg Arg Leu Met Met Ser  
 65 70 75 80  
 Lys Glu Asn Met Lys Leu Pro Gln Pro Pro Glu Gly Gln Cys Tyr Ser  
 85 90 95  
 Asn

## FIG.7F

atgaaaaccg aatatacagc cttaaataag 30

Met Lys Thr Glu Tyr Thr Ala Leu Lys  
 1 5

## FIG.7G

atgtggacct aa 12

Met Trp Thr  
 1

## FIG.7H

31/66

atgaatggag taaatagttc taatggagtg gtggacccaa gagccatatac agtgctagca 60  
 aaatggcaga attcatatag catcaaagtt gtcctgcaag agcttcggcg cctaatagatg 120  
 tctaaagaaa atatgaaact ccctcagccg cccgaaggac agtgttacag caattaa 177

Met Asn Gly Val Asn Ser Ser Asn Gly Val Val Asp Pro Arg Ala Ile  
 1 5 10 15  
 Ser Val Leu Ala Lys Trp Gln Asn Ser Tyr Ser Ile Lys Val Val Leu  
 20 25 30  
 Gln Glu Leu Arg Arg Leu Met Met Ser Lys Glu Asn Met Lys Leu Pro  
 35 40 45  
 Gln Pro Pro Glu Gly Gln Cys Tyr Ser Asn  
 50 55

FIG.7I

atggagtggt ggacccaaga gccatatacag tgctag 36

Met Glu Trp Trp Thr Gln Glu Pro Tyr Gln Cys  
 1 5 10

FIG.7J

atggcagaat tcatatag 18

Met Ala Glu Phe Ile  
 1 5  
 2

FIG.7K

atgatgtcta aagaaaatat gaaactccct cagccgcccc aaggacagtg ttacagcaat 60  
 taa 63

Met Met Ser Lys Glu Asn Met Lys Leu Pro Gln Pro Pro Glu Gly Gln  
 1 5 10 15  
 Cys Tyr Ser Asn  
 20

FIG.7L



32/66

atgtctaaag aaaatatgaa actccctcag cgcgccgaag gacagtgtta cagcaattaa 60

Met Ser Lys Glu Asn Met Lys Leu Pro Gln Pro Pro Glu Gly Gln Cys  
 1 5 10 15  
 Tyr Ser Asn

## FIG.7M

atgaaactcc ctcagccgcc cgaaggacag tgttacagca attaa 45

Met Lys Leu Pro Gln Pro Pro Glu Gly Gln Cys Tyr Ser Asn  
 1 5 10

## FIG.7N

atgatactaa ttttttcgtc catttga 27

Met Ile Leu Ile Phe Ser Ser Ile  
 1 5

## FIG.7O

atgcccttc caaaccatca tcctgtcccc acgtcctcctcc actcccgccc ttggccgaag 60  
 catagattgt aa 72

Met Pro Leu Pro Asn His His Pro Val Pro Thr Leu Leu His Ser Arg  
 1 5 10 15  
 Pro Trp Pro Lys His Arg Leu  
 20

## FIG.7P

atgacacttc cttgcttttg ccagaagcca tcaggtaagg ttggaaagag cctctga 57

Met Thr Leu Pro Cys Phe Gly Gln Lys Pro Ser Gly Lys Val Gly Lys  
 1 5 10 15  
 Ser Leu

## FIG.7Q

atgaatattg ggtcctcagc cctgccaccc tctgctgtca tcagctga 48

Met Asn Ile Gly Ser Ser Ala Leu Pro Pro Ser Ala Val Ile Ser  
 1 5 10 15

## FIG.7R

SUBSTITUTE SHEET (RULE 26)

33/66

atgcattggt ttttag 15

Met His Cys Phe

1

FIG.7S

atgaagatac ttgtaagcac acatgatccc tctgaattgt tttactttcc tgtaactgct 60  
 tttgctttta aaaattga 78

Met Lys Ile Leu Val Ser Thr His Asp Pro Ser Glu Leu Phe Tyr Phe  
 1 5 10 15  
 Pro Val Thr Ala Phe Ala Phe Lys Asn  
 20 25

FIG.7T

atgatccctc tgaattgttt tactttcctg taa 33

Met Ile Pro Leu Asn Cys Phe Thr Phe Leu

1

5

10

FIG.7U

atgccttggt tttggtgctg ctgctgcttc ccaagatcct cagcagggat taagaaggaa 60  
 cccggtgtgc acagcagatc cccgaaattg gtgggcttga cctcctggca aattgctgcg 120  
 tctttccact tgctgttcag gaccactaaa tgctga 156

Met Pro Trp Phe Trp Cys Cys Cys Cys Phe Pro Arg Ser Ser Ala Gly  
 1 5 10 15  
 Ile Lys Lys Glu Pro Gly Val His Ser Arg Ser Pro Lys Leu Val Gly  
 20 25 30  
 Leu Thr Ser Trp Gln Ile Ala Ala Ser Phe His Leu Leu Phe Arg Thr  
 35 40 45  
 Thr Lys Cys  
 50

FIG.7V

atgctgaaat gtggatgcat accgaaataa 30

Met Leu Lys Cys Gly Cys Ile Pro Lys

1

5

FIG.7W

SUBSTITUTE SHEET (RULE 26)

34/66

atgtggatgc ataccgaaat aaaagcaatt cattgtgtac taaaggtttt tttttttttt 60  
 ttaatttag 69

Met Trp Met His Thr Glu Ile Lys Ala Ile His Cys Val Leu Lys Val  
 1 5 10 15  
 Phe Phe Phe Phe Leu Ile  
 20

FIG.7X

atgcataccg aaataaaagc aattcattgt gtactaaagg tttttttttt ttttttaatt 60  
 tag 63

Met His Thr Glu Ile Lys Ala Ile His Cys Val Leu Lys Val Phe Phe  
 1 5 10 15  
 Phe Phe Leu Ile  
 20

FIG.7Y

atgtttccat taatcttttt ctgggggggaa aaccttagtt ctaaggattt aacatcctgt 60  
 aagtga 66

Met Phe Pro Leu Ile Phe Phe Trp Gly Glu Asn Leu Ser Ser Lys Asp  
 1 5 10 15  
 Leu Thr Ser Cys Lys  
 20

FIG.7Z

35/66

atgtgtgtgt gtgtgtgtat gtgtgtgttt ctgagtaagt attga 45

Met	Cys	Val	Cys	Val	Cys	Met	Cys	Val	Phe	Leu	Ser	Lys	Tyr
1				5					10				

FIG.8A

atgtgtgtgt ttctgagtaa gtattga 27

Met	Cys	Val	Phe	Leu	Ser	Lys	Tyr
1				5			

FIG.8B

atgacgaaat ga 12

Met	Thr	Lys
1		

FIG.8C

atgagatcaa taggaaatgt gctttttgag gaaattttat tttag 45

Met	Arg	Ser	Ile	Gly	Asn	Val	Leu	Phe	Glu	Glu	Ile	Leu	Phe
1				5					10				

FIG.8D

atgtgctttt tgaggaaatt ttatttttagt accaaatggt gccagtga 48

Met	Cys	Phe	Leu	Arg	Lys	Phe	Tyr	Phe	Ser	Thr	Lys	Cys	Cys	Gln
1				5					10					15

FIG.8E

atgttgccag tgacaatctt cagttaa 27

Met	Leu	Pro	Val	Thr	Ile	Phe	Ser
1				5			

FIG.8F

36/66

atgaataagc agcatttttc attgcactta aaaatgtaa 39

Met Asn Lys Gln His Phe Ser Leu His Leu Lys Met  
1 5 10

## FIG.8G

atgccactaa tctgtaacat tttaccagtt cagatgcctg taatgtgtga ctttatgtgt 60  
gtctgtgttg ttttgaagag aataaaggaa ataatacttt gcaaactggt taaacaagtg 120  
tttaaacttc tattggcaac atttattggg ctaagcagtt attga 165

Met Pro Leu Ile Cys Asn Ile Leu Pro Val Gln Met Pro Val Met Cys  
1 5 10 15  
Asp Phe Met Cys Val Cys Val Val Leu Lys Arg Ile Lys Glu Ile Ile  
20 25 30  
Leu Cys Lys Leu Phe Lys Gln Val Phe Lys Leu Leu Leu Ala Thr Phe  
35 40 45  
Ile Gly Leu Ser Ser Tyr  
50

## FIG.8H

atgcctgtaa tgtgtgactt tatgtgtgtc tgtgttggtt tgaagagaat aaaggaaata 60  
atactttgca aactgtttta acaagtgttt aaacttctat tggcaacatt tattgggcta 120  
agcagttatt ga 132

Met Pro Val Met Cys Asp Phe Met Cys Val Cys Val Val Leu Lys Arg  
1 5 10 15  
Ile Lys Glu Ile Ile Leu Cys Lys Leu Phe Lys Gln Val Phe Lys Leu  
20 25 30  
Leu Leu Ala Thr Phe Ile Gly Leu Ser Ser Tyr  
35 40

## FIG.8I

37/66

atgtgtgact ttatgtgtgt ctgtgttgtt ttgaagagaa taaaggaaat aatactttgc 60  
 aaactgttta aacaagtgtt taaacttcta ttggcaacat ttattgggct aagcagttat 120  
 tga 123

Met Cys Asp Phe Met Cys Val Cys Val Val Leu Lys Arg Ile Lys Glu  
 1 5 10 15  
 Ile Ile Leu Cys Lys Leu Phe Lys Gln Val Phe Lys Leu Leu Leu Ala  
 20 25 30  
 Thr Phe Ile Gly Leu Ser Ser Tyr  
 35 40

FIG.8J

atgtgtgtct gtgttgtttt gaagagaata aaggaaataa tactttgcaa actgtttaaa 60  
 caagtgttta aacttctatt ggcaacattt attgggctaa gcagttattg a 111

Met Cys Val Cys Val Val Leu Lys Arg Ile Lys Glu Ile Ile Leu Cys  
 1 5 10 15  
 Lys Leu Phe Lys Gln Val Phe Lys Leu Leu Leu Ala Thr Phe Ile Gly  
 20 25 30  
 Leu Ser Ser Tyr  
 35

FIG.8K

atgtgtgatg aagcaaaatg tataaagtat gaaatattat acttttacctc tggataa 57

Met Cys Asp Glu Ala Lys Cys Ile Lys Tyr Glu Ile Leu Tyr Phe Tyr  
 1 5 10 15  
 Pro Gly

FIG.8L

atgaagcaaa atgtataa 18

Met Lys Gln Asn Val  
 1 5

FIG.8M

atgtataaag tatga 15

Met Tyr Lys Val  
 1

FIG.8N

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atgaaatatt atacttttac cctggataat tattcaggac cccagttggc ccaaataagg 60  
gcaattttta atcctttgaa attagccagc cagacctaa 99

Met Lys Tyr Tyr Thr Phe Thr Leu Asp Asn Tyr Ser Gly Pro Gln Leu  
1 5 10 15  
Ala Gln Ile Gly Ala Ile Phe Asn Pro Leu Lys Leu Ala Ser Gln Thr  
20 25 30

FIG.8O

atgctaagg 12

Met Leu Arg  
1

FIG.8P

atgtatctat ttctgtcagg aatgatattt ccaaataaaa atgtaaagaa cattgggaaa 60  
taa 63

Met Tyr Leu Phe Leu Ser Gly Met Ile Phe Pro Asn Glu Asn Val Lys  
1 5 10 15  
Asn Ile Gly Lys  
20

FIG.8Q

atgatatttc caaatgaaaa tgtaaagaac attgggaaat aa 42

Met Ile Phe Pro Asn Glu Asn Val Lys Asn Ile Gly Lys  
1 5 10

FIG.8R

atgaaaatgt aa 12

Met Lys Met  
1

FIG.8S

39/66

atgaagagta acagtgtaga ccagactgcc tctctcagat atgtgcctga tattttgtgg 60  
 atacctcccc tgcactggca aaacactatg cttttgggtg ttagactgaa atattttaag 120  
 agtatTTaa 129

Met Lys Ser Asn Ser Val Asp Gln Thr Ala Ser Leu Arg Tyr Val Pro  
 1 5 10 15  
 Asp Ile Leu Trp Ile Pro Pro Leu His Trp Gln Asn Thr Met Leu Leu  
 20 25 30  
 Gly Val Arg Leu Lys Tyr Phe Lys Ser Ile  
 35 40

FIG.9A

atgtgcctga tattttgtgg atacctcccc tgcactggca aaacactatg cttttgggtg 60  
 ttagactga 69

Met Cys Leu Ile Phe Cys Gly Tyr Leu Pro Cys Thr Gly Lys Thr Leu  
 1 5 10 15  
 Cys Phe Trp Val Leu Asp  
 20

FIG.9B

atgcttttgg gtgtagact gaaatatttt aagagtattt aa 42

Met Leu Leu Gly Val Arg Leu Lys Tyr Phe Lys Ser Ile  
 1 5 10

FIG.9C

atggaaatgt atcttatgaa tagagacata ttaaaataa 39

Met Glu Met Tyr Leu Met Asn Arg Asp Ile Leu Lys  
 1 5 10

FIG.9D

atgtatctta tgaatagaga catattaaaa taa 33

Met Tyr Leu Met Asn Arg Asp Ile Leu Lys  
 1 5 10

FIG.9E



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atgaatagag acatattaaa ataa 24

Met Asn Arg Asp Ile Leu Lys

1

5

FIG.9F

atgtttacat cttag 15

Met Phe Thr Ser

1

FIG.9G

atggtttctg gagacaaata a 21

Met Val Ser Gly Asp Lys

1

5

FIG.9H

atgatttatt ttttgactaa atgtgcaatt tcttatcact ag 42

Met Ile Tyr Phe Leu Thr Lys Cys Ala Ile Ser Tyr His

1

5

10

FIG.9I

atgtgcaatt tcttatcact agataacttt cagtatcagt ggtggttact tattacttaa 60

Met Cys Asn Phe Leu Ser Leu Asp Asn Phe Gln Tyr Gln Trp Trp Leu

1

5

10

15

Leu Ile Thr

FIG.9J

atgtcgactt gctaa 15

Met Ser Thr Cys

1

FIG.9K

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atgtcttttt ttttagtgtc ccaaagatat cttagataa 39

Met	Ser	Phe	Phe	Leu	Val	Ser	Gln	Arg	Tyr	Leu	Arg
1				5					10		

FIG.9L

atgaggcaac	attttcttga	gataattacc	caagtttcat	ccatgttgaa	tggtacaaaa	60
tatttctgtg	aaactaacag	gaagatattt	tcagataact	ag		102

Met	Arg	Gln	His	Phe	Leu	Glu	Ile	Ile	Thr	Gln	Val	Ser	Ser	Met	Leu
1				5					10					15	
Asn	Gly	Thr	Lys	Tyr	Phe	Cys	Glu	Thr	Asn	Arg	Lys	Ile	Phe	Ser	Asp
			20					25					30		

Asn

FIG.9M

atgttgaatg gtacaaaata tttctgtgaa actaacagga agatattttc agataactag 60

Met	Leu	Asn	Gly	Thr	Lys	Tyr	Phe	Cys	Glu	Thr	Asn	Arg	Lys	Ile	Phe
1				5					10					15	
Ser	Asp	Asn													

FIG.9N

atggtacaaa	atatttctgt	gaaactaaca	ggaagatatt	ttcagataac	taggataact	60
tggtgctttg	ttacccagcc	taattga				87

Met	Val	Gln	Asn	Ile	Ser	Val	Lys	Leu	Thr	Gly	Arg	Tyr	Phe	Gln	Ile
1				5					10					15	
Thr	Arg	Ile	Thr	Cys	Cys	Phe	Val	Thr	Gln	Pro	Asn				
			20					25							

FIG.9O

42/66

atgcttgttt caaagaacca acagaaaaaa aagctaagaa aactgagaac taacattaaa 60  
 aaaattaaat ttagaataag aatgatttct ttaatttgct ctttttttct ttgggtctaaa 120  
 acattattaa atttttgtaa atattttgat ttaatgtgtc ttagatcctc attatttta 180

Met Leu Val Ser Lys Asn Gln Gln Lys Lys Lys Leu Arg Lys Leu Arg  
 1 5 10 15  
 Thr Asn Ile Lys Lys Ile Lys Phe Arg Ile Arg Met Ile Ser Leu Ile  
 20 25 30  
 Cys Pro Phe Phe Leu Trp Ser Lys Thr Leu Leu Asn Phe Cys Lys Tyr  
 35 40 45  
 Phe Asp Leu Met Cys Leu Arg Ser Ser Leu Phe  
 50 55

FIG.9P

atgatttctt taatttgctc tttttttctt tgggtctaaaa cattattaaa tttttgtaaa 60  
 tattttgatt taatgtgtct tagatcctca ttatttta 99

Met Ile Ser Leu Ile Cys Pro Phe Phe Leu Trp Ser Lys Thr Leu Leu  
 1 5 10 15  
 Asn Phe Cys Lys Tyr Phe Asp Leu Met Cys Leu Arg Ser Ser Leu Phe  
 20 25 30

FIG.9Q

atgtgtctta gatcctcatt atttta 27

Met Cys Leu Arg Ser Ser Leu Phe  
 1 5

FIG.9R

atgctaatat gtaaagttca tgccatccag gcatttaaga gcgatcctca tcccttcagc 60  
 aatatgtatt tgagttcaca ctatttctgt tttacagcag ttttgaaaaa cacatactat 120  
 gccaccaatt gtcataattat ttttagatga 150

Met Leu Ile Cys Lys Val His Ala Ile Gln Ala Phe Lys Ser Asp Pro  
 1 5 10 15  
 His Pro Phe Ser Asn Met Tyr Leu Ser Ser His Tyr Phe Cys Phe Thr  
 20 25 30  
 Ala Val Leu Lys Asn Thr Tyr Tyr Ala Thr Asn Cys His Ile Ile Phe  
 35 40 45  
 Arg

FIG.9S

SUBSTITUTE SHEET (RULE 26)

43/66

atgccatcca ggcatTTaag agcgatcctc atcccttcag caatatgtat ttga 54

Met Pro Ser Arg His Leu Arg Ala Ile Leu Ile Pro Ser Ala Ile Cys  
 1 5 10 15  
 Ile

## FIG.9T

atgtatttga gttcacacta tttctgtttt acagcagttt tgaaaaacac atactatgcc 60  
 accaattgtc atattatttt tagatga 87

Met Tyr Leu Ser Ser His Tyr Phe Cys Phe Thr Ala Val Leu Lys Asn  
 1 5 10 15  
 Thr Tyr Tyr Ala Thr Asn Cys His Ile Ile Phe Arg  
 20 25

## FIG.9U

atgccaccaa ttgtcatatt atttttagat gatgtaacat ag 42

Met Pro Pro Ile Val Ile Leu Phe Leu Asp Asp Val Thr  
 1 5 10

## FIG.9V

atgcctaata cttag 15

Met Pro Asn Thr  
 1

## FIG.9W

atgtcacgag atcattttta cattaaacgt gaaaaaaaaat caaaaaaaaa aaaaaaaaaa 60  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 120  
 aaaaaaaaaa agggcgcc 139

Met Ser Arg Asp His Phe Tyr Ile Lys Arg Glu Lys Lys Ser Lys Lys  
 1 5 10 15  
 Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys  
 20 25 30  
 Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Gly  
 35 40 45

## FIG.9X

44/66

```

atgagccggc aggtggtccg ctccagcaag ttccgccacg tgtttggaca gccggccaag 60
gccgaccagt gctatgaaga tgtgcgcgtc tcacagacca cctgggacag tggcttctgt 120
gctgtcaacc ctaagtttgt ggccctgata tgtgaggcca gcgggggagg ggccttctgt 180
gtgctgcccc tgggcaagac tggacgtgtg gacaagaatg cggccacggt ctgtggccac 240
acagcccctg tgctagacat cgcctggtgc ccgcacaatg acaacgtcat tgccagtggc 300
tccgaggact gcacagtcac ggtgtgggag atcccagatg ggggcctgat gctgcccctg 360
cgggagcccc tcgtcacctt ggagggccac accaagcgtg tgggcattgt ggcctggcac 420
accacagccc agaacgtgct gctcagtga ggttgtgaca acgtgatcat ggtgtgggac 480
gtgggcactg gggcgcccat gctgacactg ggcccagagg tgcaccaga cacgatctac 540
agtgtggact ggagccgaga tggaggcctc atttgtacct cctgccgtga caagcgcgtg 600
cgcacatcag agccccgcaa aggcactgtc gtagctgaga aggaccgtcc ccacgagggg 660
acccggcccc tgcgtgcagt gttcgtgtcg gaggggaaga tcctgaccac gggcttcagc 720
cgcatgagtg agcggcaggt ggcgtgtgtg gacacaaagc acctggagga gccgtgtgtc 780
ctgcaggagc tggacaccag cagcgtgtgc ctgctgccct tctttgacct tgacaccaac 840
atcgtctacc tctgtggcaa ggggtgacagc tcaatccggt actttgagat cacttccgag 900
gcccctttcc tgcactatct ctccatgttc agttccaagg agtcccagcg gggcatgggc 960
tacatgcccc aacgtggcct ggaggtgaac aagtgtgaga tcgccagggt ctacaagctg 1020
cacgagcgga ggtgtgagcc cattgccatg acagtgcctc gaaagtcgga cctgttccag 1080
gaggacctgt acccaccacac egcagggccc gaccctgccc tcacggctga ggagtggctg 1140
gggggtcggg atgctgggcc cctcctcatc tccctcaagg atggctacgt acccccaaag 1200
agccgggagc tgaggggtcaa ccggggcctg gacaccgggc gcaggagggc agcaccagag 1260
gccagtggca ctcccagctc ggatgccgtg tctcggctgg aggaggagat gcggaagctc 1320
caggccacgg tgcaggagct ccagaagcgc ttggacaggc tggaggagac agtccaggcc 1380
aagtag

```

```

Met Ser Arg Gln Val Val Arg Ser Ser Lys Phe Arg His Val Phe Gly
 1           5           10           15
Gln Pro Ala Lys Ala Asp Gln Cys Tyr Glu Asp Val Arg Val Ser Gln
          20           25           30
Thr Thr Trp Asp Ser Gly Phe Cys Ala Val Asn Pro Lys Phe Val Ala
          35           40           45
Leu Ile Cys Glu Ala Ser Gly Gly Gly Ala Phe Leu Val Leu Pro Leu
          50           55           60
Gly Lys Thr Gly Arg Val Asp Lys Asn Ala Pro Thr Val Cys Gly His
65           70           75           80
Thr Ala Pro Val Leu Asp Ile Ala Trp Cys Pro His Asn Asp Asn Val
          85           90           95
Ile Ala Ser Gly Ser Glu Asp Cys Thr Val Met Val Trp Glu Ile Pro
          100          105          110
Asp Gly Gly Leu Met Leu Pro Leu Arg Glu Pro Val Val Thr Leu Glu
          115          120          125
Gly His Thr Lys Arg Val Gly Ile Val Ala Trp His Thr Thr Ala Gln
          130          135          140

```

FIG. 10A-1

SUBSTITUTE SHEET (RULE 26)

45/66

Asn Val Leu Leu Ser Ala Gly Cys Asp Asn Val Ile Met Val Trp Asp																			
145				150				155											160
Val Gly Thr Gly Ala Ala Met Leu Thr Leu Gly Pro Glu Val His Pro				165				170											175
Asp Thr Ile Tyr Ser Val Asp Trp Ser Arg Asp Gly Gly Leu Ile Cys				180				185											190
Thr Ser Cys Arg Asp Lys Arg Val Arg Ile Ile Glu Pro Arg Lys Gly				195				200											205
Thr Val Val Ala Glu Lys Asp Arg Pro His Glu Gly Thr Arg Pro Val				210				215											220
Arg Ala Val Phe Val Ser Glu Gly Lys Ile Leu Thr Thr Gly Phe Ser				225				230											240
Arg Met Ser Glu Arg Gln Val Ala Leu Trp Asp Thr Lys His Leu Glu				245				250											255
Glu Pro Leu Ser Leu Gln Glu Leu Asp Thr Ser Ser Gly Val Leu Leu				260				265											270
Pro Phe Phe Asp Pro Asp Thr Asn Ile Val Tyr Leu Cys Gly Lys Gly				275				280											285
Asp Ser Ser Ile Arg Tyr Phe Glu Ile Thr Ser Glu Ala Pro Phe Leu				290				295											300
His Tyr Leu Ser Met Phe Ser Ser Lys Glu Ser Gln Arg Gly Met Gly				305				310											320
Tyr Met Pro Lys Arg Gly Leu Glu Val Asn Lys Cys Glu Ile Ala Arg				325				330											335
Phe Tyr Lys Leu His Glu Arg Arg Cys Glu Pro Ile Ala Met Thr Val				340				345											350
Pro Arg Lys Ser Asp Leu Phe Gln Glu Asp Leu Tyr Pro Pro Thr Ala				355				360											365
Gly Pro Asp Pro Ala Leu Thr Ala Glu Glu Trp Leu Gly Gly Arg Asp				370				375											380
Ala Gly Pro Leu Leu Ile Ser Leu Lys Asp Gly Tyr Val Pro Pro Lys				385				390											400
Ser Arg Glu Leu Arg Val Asn Arg Gly Leu Asp Thr Gly Arg Arg Arg				405				410											415
Ala Ala Pro Glu Ala Ser Gly Thr Pro Ser Ser Asp Ala Val Ser Arg				420				425											430
Leu Glu Glu Glu Met Arg Lys Leu Gln Ala Thr Val Gln Glu Leu Gln				435				440											445
Lys Arg Leu Asp Arg Leu Glu Glu Thr Val Gln Ala Lys				450				455											460

FIG. 10A-2

46/66

atgaagatgt ggcgctctca cagaccacct gggacagtgg cttctgtgct gtcaacccta 60  
agtttgtggc cctga 75

Met Lys Met Cys Ala Ser His Arg Pro Pro Gly Thr Val Ala Ser Val  
1 5 10 15  
Leu Ser Thr Leu Ser Leu Trp Pro  
20

## FIG. 10B

atgtgcgcgt ctcacagacc acctgggaca gtggcttctg tgctgtcaac cctaagtttg 60  
tggccctga 69

Met Cys Ala Ser His Arg Pro Pro Gly Thr Val Ala Ser Val Leu Ser  
1 5 10 15  
Thr Leu Ser Leu Trp Pro  
20

## FIG. 10C

atgcgcccac ggtctgtggc cacacagccc ctgtgctag 39

Met Arg Pro Arg Ser Val Ala Thr Gln Pro Leu Cys  
1 5 10

## FIG. 10D

atgacaacgt cattgccagt ggctccgagg actgcacagt catggtgtgg gagatcccag 60  
atgggggcct ga 72

Met Thr Thr Ser Leu Pro Val Ala Pro Arg Thr Ala Gln Ser Trp Cys  
1 5 10 15  
Gly Arg Ser Gln Met Gly Ala  
20

## FIG. 10E

47/66

```

atggtgtggg agatcccaga tgggggcctg atgctgcccc tgcgggagcc cgtcgtcacc 60
ctggagggcc acaccaagcg tgtgggcatt gtggcctggc acaccacagc ccagaacgtg 120
ctgctcagtg caggttgtga caacgtgatc atggtgtggg acgtgggcac tggggcggcc 180
atgctgacac tgggcccaga ggtgcacca gacacgatct acagtgtgga ctggagccga 240
gatggaggcc tcatttgtac ctcctgccgt gacaagcgcg tgcgcatcat cgagccccgc 300
aaaggcactg tcgtagctga gaaggaccgt cccacagagg ggaccggcc cgtgctgca 360
gtgttcgtgt cggaggggaa gatcctgacc acgggcttca gccgcatgag tgagcggcag 420
gtggcgctgt gggacacaaa gcacctggag gagccgctgt ccctgcagga gctggacacc 480
agcagcgggtg tcctgctgcc cttctttgac cctgacacca acatcgtcta cctctgtggc 540
aagggtgaca gctcaatccg gtactttgag atcacttccg agggcccttt cctgcactat 600
ctctccatgt tcagttccaa ggagtcccag cggggcatgg gctacatgcc caaacgtggc 660
ctggaggtga acaagtgtga gatcgccagg ttctacaagc tgcacgagcg gaggtgtgag 720
cccattgcca tgacagtgcc tcgaaagtcg gacctgttcc aggaggacct gtaccaccc 780
accgcagggc ccgaccctgc cctcacggct gaggagtggc tggggggctg ggatgctggg 840
cccctcctca tctccctcaa ggatggctac gtaccccaa agagccggga gctgagggtc 900
aaccggggcc tggacaccgg gcgcaggagg gcagcaccag aggccagtgg cactcccagc 960
tcggatgccg tgtctcggct ggaggaggag atgcggaagc tccaggccac ggtgcaggag 1020
ctccagaagc gcttggacag gctggaggag acagtccagg ccaagtag 1068

```

```

Met Val Trp Glu Ile Pro Asp Gly Gly Leu Met Leu Pro Leu Arg Glu
 1           5           10           15
Pro Val Val Thr Leu Glu Gly His Thr Lys Arg Val Gly Ile Val Ala
      20           25           30
Trp His Thr Thr Ala Gln Asn Val Leu Leu Ser Ala Gly Cys Asp Asn
      35           40           45
Val Ile Met Val Trp Asp Val Gly Thr Gly Ala Ala Met Leu Thr Leu
      50           55           60
Gly Pro Glu Val His Pro Asp Thr Ile Tyr Ser Val Asp Trp Ser Arg
65           70           75           80
Asp Gly Gly Leu Ile Cys Thr Ser Cys Arg Asp Lys Arg Val Arg Ile
      85           90           95
Ile Glu Pro Arg Lys Gly Thr Val Val Ala Glu Lys Asp Arg Pro His
      100          105          110
Glu Gly Thr Arg Pro Val Arg Ala Val Phe Val Ser Glu Gly Lys Ile
      115          120          125
Leu Thr Thr Gly Phe Ser Arg Met Ser Glu Arg Gln Val Ala Leu Trp
      130          135          140
Asp Thr Lys His Leu Glu Glu Pro Leu Ser Leu Gln Glu Leu Asp Thr
145          150          155          160
Ser Ser Gly Val Leu Leu Pro Phe Phe Asp Pro Asp Thr Asn Ile Val
      165          170          175

```

FIG. 10F-1



48/66

Tyr Leu Cys Gly Lys Gly Asp Ser Ser Ile Arg Tyr Phe Glu Ile Thr  
 180 185 190  
 Ser Glu Ala Pro Phe Leu His Tyr Leu Ser Met Phe Ser Ser Lys Glu  
 195 200 205  
 Ser Gln Arg Gly Met Gly Tyr Met Pro Lys Arg Gly Leu Glu Val Asn  
 210 215 220  
 Lys Cys Glu Ile Ala Arg Phe Tyr Lys Leu His Glu Arg Arg Cys Glu  
 225 230 235 240  
 Pro Ile Ala Met Thr Val Pro Arg Lys Ser Asp Leu Phe Gln Glu Asp  
 245 250 255  
 Leu Tyr Pro Pro Thr Ala Gly Pro Asp Pro Ala Leu Thr Ala Glu Glu  
 260 265 270  
 Trp Leu Gly Gly Arg Asp Ala Gly Pro Leu Leu Ile Ser Leu Lys Asp  
 275 280 285  
 Gly Tyr Val Pro Pro Lys Ser Arg Glu Leu Arg Val Asn Arg Gly Leu  
 290 295 300  
 Asp Thr Gly Arg Arg Arg Ala Ala Pro Glu Ala Ser Gly Thr Pro Ser  
 305 310 315 320  
 Ser Asp Ala Val Ser Arg Leu Glu Glu Glu Met Arg Lys Leu Gln Ala  
 325 330 335  
 Thr Val Gln Glu Leu Gln Lys Arg Leu Asp Arg Leu Glu Glu Thr Val  
 340 345 350  
 Gln Ala Lys  
 355

FIG. 10F-2

atgggggcct ga 12

Met Gly Ala

1

FIG. 10G

49/66

```

atgctgcccc tgcgggagcc cgtcgtcacc ctggagggcc acaccaagcg tgtgggcatt 60
gtggcctggc acaccacagc ccagaacgtg ctgctcagtg caggttgtga caacgtgatc 120
atggtgtggg acgtgggcac tggggcggcc atgctgacac tgggcccaga ggtgcaccca 180
gacacgatct acagtgtgga ctggagccga gatggaggcc tcatttgtac ctctgccgt 240
gacaagcgcg tgcgcatcat cgagcccgcc aaaggcactg tcgtagctga gaaggaccgt 300
ccccacgagg ggacccggcc cgtgcgtgca gtgttcgtgt cggaggggaa gatcctgacc 360
acgggcttca gccgcatgag tgagcggcag gtggcgctgt gggacacaaa gcacctggag 420
gagccgctgt ccctgcagga gctggacacc agcagcgggtg tcctgctgcc cttctttgac 480
cctgacacca acatcgtcta cctctgtggc aagggtgaca gctcaatccg gtactttgag 540
atcacttccg agggcccttt cctgcactat ctctccatgt tcagttccaa ggagtcccag 600
cggggcatgg gctacatgcc caaacgtggc ctggaggtga acaagtgtga gatcgccagg 660
ttctacaagc tgcacgagcg gaggtgtgag cccattgcc a tgacagtgcc tcgaaagtcg 720
gacctgttcc aggaggacct gtaccacacc accgcagggc ccgaccctgc cctcacggct 780
gaggagtggc tggggggtcg ggatgctggg cccctcctca tctccctcaa ggatggctac 840
gtacccccaa agagccggga gctgaggggtc aaccggggcc tggacaccgg gcgcaggagg 900
gcagcaccag aggccagtgg cactcccagc tcggatgccg tgtctcggct ggaggaggag 960
atgcggaagc tccaggccac ggtgcaggag ctccagaagc gcttggacag gctggaggag 1020
acagtccagg ccaagtag                                     1038

```

```

Met Leu Pro Leu Arg Glu Pro Val Val Thr Leu Glu Gly His Thr Lys
 1           5           10          15
Arg Val Gly Ile Val Ala Trp His Thr Thr Ala Gln Asn Val Leu Leu
      20           25           30
Ser Ala Gly Cys Asp Asn Val Ile Met Val Trp Asp Val Gly Thr Gly
      35           40           45
Ala Ala Met Leu Thr Leu Gly Pro Glu Val His Pro Asp Thr Ile Tyr
      50           55           60
Ser Val Asp Trp Ser Arg Asp Gly Gly Leu Ile Cys Thr Ser Cys Arg
65           70           75           80
Asp Lys Arg Val Arg Ile Ile Glu Pro Arg Lys Gly Thr Val Val Ala
      85           90           95
Glu Lys Asp Arg Pro His Glu Gly Thr Arg Pro Val Arg Ala Val Phe
      100          105          110
Val Ser Glu Gly Lys Ile Leu Thr Thr Gly Phe Ser Arg Met Ser Glu
      115          120          125
Arg Gln Val Ala Leu Trp Asp Thr Lys His Leu Glu Pro Leu Ser
      130          135          140
Leu Gln Glu Leu Asp Thr Ser Ser Gly Val Leu Leu Pro Phe Phe Asp
145          150          155          160
Pro Asp Thr Asn Ile Val Tyr Leu Cys Gly Lys Gly Asp Ser Ser Ile
      165          170          175

```

FIG. 10H-1

50/66

Arg	Tyr	Phe	Glu	Ile	Thr	Ser	Glu	Ala	Pro	Phe	Leu	His	Tyr	Leu	Ser
			180					185					190		
Met	Phe	Ser	Ser	Lys	Glu	Ser	Gln	Arg	Gly	Met	Gly	Tyr	Met	Pro	Lys
		195					200					205			
Arg	Gly	Leu	Glu	Val	Asn	Lys	Cys	Glu	Ile	Ala	Arg	Phe	Tyr	Lys	Leu
	210					215					220				
His	Glu	Arg	Arg	Cys	Glu	Pro	Ile	Ala	Met	Thr	Val	Pro	Arg	Lys	Ser
225					230					235					240
Asp	Leu	Phe	Gln	Glu	Asp	Leu	Tyr	Pro	Pro	Thr	Ala	Gly	Pro	Asp	Pro
				245						250				255	
Ala	Leu	Thr	Ala	Glu	Glu	Trp	Leu	Gly	Gly	Arg	Asp	Ala	Gly	Pro	Leu
			260					265					270		
Leu	Ile	Ser	Leu	Lys	Asp	Gly	Tyr	Val	Pro	Pro	Lys	Ser	Arg	Glu	Leu
		275					280						285		
Arg	Val	Asn	Arg	Gly	Leu	Asp	Thr	Gly	Arg	Arg	Arg	Ala	Ala	Pro	Glu
		290				295						300			
Ala	Ser	Gly	Thr	Pro	Ser	Ser	Asp	Ala	Val	Ser	Arg	Leu	Glu	Glu	Glu
305					310					315					320
Met	Arg	Lys	Leu	Gln	Ala	Thr	Val	Gln	Glu	Leu	Gln	Lys	Arg	Leu	Asp
				325					330					335	
Arg	Leu	Glu	Glu	Thr	Val	Gln	Ala	Lys							
			340					345							

FIG. 10H-2

51/66

```

atggtgtggg acgtgggcac tggggcggcc atgctgacac tggggcccaga ggtgcaccca 60
gacacgatct acagtgtgga ctggagccga gatggaggcc tcatttgtac ctctgccgt 120
gacaagcgcg tgcgcatcat cgagccccgc aaaggcactg tcgtagctga gaaggaccgt 180
ccccacgagg ggacccggcc cgtgcgtgca gtgttcgtgt cggaggggaa gatcctgacc 240
acgggcttca gccgcatgag tgagcggcag gtggcgctgt gggacacaaa gcacctggag 300
gagccgctgt ccctgcagga gctggacacc agcagcgggtg tcctgctgcc cttctttgac 360
cctgacacca acatcgtcta cctctgtggc aagggtgaca gctcaatccg gtactttgag 420
atcacttccg aggccccctt cctgcactat ctctccatgt tcagttccaa ggagtccag 480
cggggcatgg gctacatgcc caaacgtggc ctggaggtga acaagtgtga gatcgccagg 540
ttctacaagc tgcacgagcg gaggtgtgag cccattgcc a tgacagtgcc tcgaaagtcg 600
gacctgttcc aggaggacct gtaccacacc accgcagggc ccgaccctgc cctcacggct 660
gaggagtggc tggggggctg ggatgctggg cccctcctca tctccctcaa ggatggctac 720
gtacccccaa agagccggga gctgaggggtc aaccggggcc tggacaccgg gcgcaggagg 780
gcagcaccag aggccagtgg cactcccagc tcggatgccg tgtctcggct ggaggaggag 840
atgcggaagc tccaggccac ggtgcaggag ctccagaagc gcttggacag gctggaggag 900
acagtccagg ccaagtag
918

```

```

Met Val Trp Asp Val Gly Thr Gly Ala Ala Met Leu Thr Leu Gly Pro
1      5      10      15
Glu Val His Pro Asp Thr Ile Tyr Ser Val Asp Trp Ser Arg Asp Gly
20     25     30
Gly Leu Ile Cys Thr Ser Cys Arg Asp Lys Arg Val Arg Ile Ile Glu
35     40     45
Pro Arg Lys Gly Thr Val Val Ala Glu Lys Asp Arg Pro His Glu Gly
50     55     60
Thr Arg Pro Val Arg Ala Val Phe Val Ser Glu Gly Lys Ile Leu Thr
65     70     75     80
Thr Gly Phe Ser Arg Met Ser Glu Arg Gln Val Ala Leu Trp Asp Thr
85     90     95
Lys His Leu Glu Glu Pro Leu Ser Leu Gln Glu Leu Asp Thr Ser Ser
100    105    110
Gly Val Leu Leu Pro Phe Phe Asp Pro Asp Thr Asn Ile Val Tyr Leu
115    120    125
Cys Gly Lys Gly Asp Ser Ser Ile Arg Tyr Phe Glu Ile Thr Ser Glu
130    135    140
Ala Pro Phe Leu His Tyr Leu Ser Met Phe Ser Ser Lys Glu Ser Gln
145    150    155    160
Arg Gly Met Gly Tyr Met Pro Lys Arg Gly Leu Glu Val Asn Lys Cys
165    170    175
Glu Ile Ala Arg Phe Tyr Lys Leu His Glu Arg Arg Cys Glu Pro Ile
180    185    190

```

FIG. 10I-1

52/66

Ala	Met	Thr	Val	Pro	Arg	Lys	Ser	Asp	Leu	Phe	Gln	Glu	Asp	Leu	Tyr
	195						200					205			
Pro	Pro	Thr	Ala	Gly	Pro	Asp	Pro	Ala	Leu	Thr	Ala	Glu	Glu	Trp	Leu
	210					215					220				
Gly	Gly	Arg	Asp	Ala	Gly	Pro	Leu	Leu	Ile	Ser	Leu	Lys	Asp	Gly	Tyr
225					230					235					240
Val	Pro	Pro	Lys	Ser	Arg	Glu	Leu	Arg	Val	Asn	Arg	Gly	Leu	Asp	Thr
			245						250					255	
Gly	Arg	Arg	Arg	Ala	Ala	Pro	Glu	Ala	Ser	Gly	Thr	Pro	Ser	Ser	Asp
			260					265					270		
Ala	Val	Ser	Arg	Leu	Glu	Glu	Glu	Met	Arg	Lys	Leu	Gln	Ala	Thr	Val
	275						280					285			
Gln	Glu	Leu	Gln	Lys	Arg	Leu	Asp	Arg	Leu	Glu	Glu	Thr	Val	Gln	Ala
	290					295					300				
Lys															
305															

FIG.10I-2

53/66

```

atgctgacac tgggcccaga ggtgcaccca gacacgatct acagtgtgga ctggagccga 60
gatggaggcc tcatttgtac ctctgccgt gacaagcgcg tgcgcatcat cgagccccgc 120
aaaggcactg tcgtagctga gaaggaccgt cccacgagg ggacccggcc cgtgcgtgca 180
gtgttcgtgt cggaggggaa gatcctgacc acgggcttca gccgcatgag tgagcggcag 240
gtggcgctgt gggacacaaa gcacctggag gagccgctgt ccctgcagga gctggacacc 300
agcagcgggtg tcctgctgcc ctcttttgac cctgacacca acatcgtcta cctctgtggc 360
aagggtgaca gctcaatccg gtactttgag atcacttccg aggccccttt cctgcactat 420
ctctccatgt tcagttccaa ggagtcccag cggggcatgg gctacatgcc caaacgtggc 480
ctggaggtga acaagtgtga gatcgccagg ttctacaagc tgcacgagcg gaggtgtgag 540
cccattgcc a tgacagtgcc tcgaaagtcg gacctgttcc aggaggacct gtaccacacc 600
accgcagggc ccgaccctgc cctcacggct gaggagtggc tggggggtcg ggatgctggg 660
ccctcctca tctccctcaa ggatggctac gtaccccaaa agagccggga gctgagggtc 720
aaccggggcc tggacaccgg gcgcaggagg gcagcaccag aggccagtgg cactcccagc 780
tcggatgccg tgtctcggct ggaggaggag atgcggaagc tccaggccac ggtgcaggag 840
ctccagaagc gcttggacag gctggaggag acagtccagg ccaagtag 888

```

```

Met Leu Thr Leu Gly Pro Glu Val His Pro Asp Thr Ile Tyr Ser Val
 1           5           10           15
Asp Trp Ser Arg Asp Gly Gly Leu Ile Cys Thr Ser Cys Arg Asp Lys
          20           25           30
Arg Val Arg Ile Ile Glu Pro Arg Lys Gly Thr Val Val Ala Glu Lys
          35           40           45
Asp Arg Pro His Glu Gly Thr Arg Pro Val Arg Ala Val Phe Val Ser
          50           55           60
Glu Gly Lys Ile Leu Thr Thr Gly Phe Ser Arg Met Ser Glu Arg Gln
65           70           75           80
Val Ala Leu Trp Asp Thr Lys His Leu Glu Glu Pro Leu Ser Leu Gln
          85           90           95
Glu Leu Asp Thr Ser Ser Gly Val Leu Leu Pro Phe Phe Asp Pro Asp
          100          105          110
Thr Asn Ile Val Tyr Leu Cys Gly Lys Gly Asp Ser Ser Ile Arg Tyr
          115          120          125
Phe Glu Ile Thr Ser Glu Ala Pro Phe Leu His Tyr Leu Ser Met Phe
          130          135          140
Ser Ser Lys Glu Ser Gln Arg Gly Met Gly Tyr Met Pro Lys Arg Gly
145          150          155          160
Leu Glu Val Asn Lys Cys Glu Ile Ala Arg Phe Tyr Lys Leu His Glu
          165          170          175
Arg Arg Cys Glu Pro Ile Ala Met Thr Val Pro Arg Lys Ser Asp Leu
          180          185          190
Phe Gln Glu Asp Leu Tyr Pro Pro Thr Ala Gly Pro Asp Pro Ala Leu
          195          200          205

```

FIG. 10J-1

SUBSTITUTE SHEET (RULE 26)

54/66

Thr Ala Glu Glu Trp Leu Gly Gly Arg Asp Ala Gly Pro Leu Leu Ile  
 210 215 220  
 Ser Leu Lys Asp Gly Tyr Val Pro Pro Lys Ser Arg Glu Leu Arg Val  
 225 230 235 240  
 Asn Arg Gly Leu Asp Thr Gly Arg Arg Arg Ala Ala Pro Glu Ala Ser  
 245 250 255  
 Gly Thr Pro Ser Ser Asp Ala Val Ser Arg Leu Glu Glu Glu Met Arg  
 260 265 270  
 Lys Leu Gln Ala Thr Val Gln Glu Leu Gln Lys Arg Leu Asp Arg Leu  
 275 280 285  
 Glu Glu Thr Val Gln Ala Lys  
 290 295

FIG.10J-2

atggaggcct catttgtacc tcctgccgtg acaagcgcgt gcgcatcatc gagccccgca 60  
 aaggcactgt cgtag 75

Met Glu Ala Ser Phe Val Pro Pro Ala Val Thr Ser Ala Cys Ala Ser  
 1 5 10 15  
 Ser Ser Pro Ala Lys Ala Leu Ser  
 20

FIG.10K

55/66

```

atgagtgagc ggcaggtggc gctgtgggac acaaagcacc tggaggagcc gctgtccctg 60
caggagctgg acaccagcag cgggtgtcctg ctgcccttct ttgaccctga caccaacatc 120
gtctacctct gtggcaaggg tgacagctca atccggtact ttgagatcac ttccgaggcc 180
cctttcctgc actatctctc catgttcagt tccaaggagt cccagcgggg catgggctac 240
atgcccaaac gtggcctgga ggtgaacaag tgtgagatcg ccagggttcta caagctgcac 300
gagcggaggt gtgagcccat tgccatgaca gtgcctcgaa agtcggacct gttccaggag 360
gacctgtacc caccaccgc agggcccgac cctgccctca cggctgagga gtggctgggg 420
ggtcgggatg ctgggcccct cctcatctcc ctcaaggatg gctacgtacc cccaaagagc 480
cgggagctga gggtaaccg gggcctggac accgggcgca ggagggcagc accagaggcc 540
agtggcactc ccagctcgga tgccgtgtct cggctggagg aggagatgcg gaagctccag 600
gccacggtgc aggagctcca gaagcgcttg gacaggctgg aggagacagt ccaggccaag 660
tag 663

```

```

Met Ser Glu Arg Gln Val Ala Leu Trp Asp Thr Lys His Leu Glu Glu
1           5           10           15
Pro Leu Ser Leu Gln Glu Leu Asp Thr Ser Ser Gly Val Leu Leu Pro
20           25           30
Phe Phe Asp Pro Asp Thr Asn Ile Val Tyr Leu Cys Gly Lys Gly Asp
35           40           45
Ser Ser Ile Arg Tyr Phe Glu Ile Thr Ser Glu Ala Pro Phe Leu His
50           55           60
Tyr Leu Ser Met Phe Ser Ser Lys Glu Ser Gln Arg Gly Met Gly Tyr
65           70           75           80
Met Pro Lys Arg Gly Leu Glu Val Asn Lys Cys Glu Ile Ala Arg Phe
85           90           95
Tyr Lys Leu His Glu Arg Arg Cys Glu Pro Ile Ala Met Thr Val Pro
100          105          110
Arg Lys Ser Asp Leu Phe Gln Glu Asp Leu Tyr Pro Pro Thr Ala Gly
115          120          125
Pro Asp Pro Ala Leu Thr Ala Glu Glu Trp Leu Gly Gly Arg Asp Ala
130          135          140
Gly Pro Leu Leu Ile Ser Leu Lys Asp Gly Tyr Val Pro Pro Lys Ser
145          150          155          160
Arg Glu Leu Arg Val Asn Arg Gly Leu Asp Thr Gly Arg Arg Arg Ala
165          170          175
Ala Pro Glu Ala Ser Gly Thr Pro Ser Ser Asp Ala Val Ser Arg Leu
180          185          190
Glu Glu Glu Met Arg Lys Leu Gln Ala Thr Val Gln Glu Leu Gln Lys
195          200          205
Arg Leu Asp Arg Leu Glu Glu Thr Val Gln Ala Lys
210          215          220

```

FIG. 10L



56/66

```

atgttcagtt ccaaggagtc ccagcggggc atgggctaca tgcccaaacg tggcctggag   60
gtgaacaagt gtgagatcgc caggttctac aagctgcacg agcggagggtg tgagccatt  120
gccatgacag tgcctcgaaa gtcggacctg ttccaggagg acctgtaccc acccaccgca  180
gggcccgcacc ctgccctcac ggctgaggag tggctggggg gtcgggatgc tgggcccctc  240
ctcatctccc tcaaggatgg ctacgtaccc ccaaagagcc gggagctgag ggtcaaccgg  300
ggcctggaca ccgggcgcag gagggcagca ccagaggcca gtggcactcc cagctcggat  360
gccgtgtctc ggctggagga ggagatgcgg aagctccagg ccacggtgca ggagctccag  420
aagcgcttgg acaggctgga ggagacagtc caggccaagt ag                        462

```

```

Met Phe Ser Ser Lys Glu Ser Gln Arg Gly Met Gly Tyr Met Pro Lys
 1           5           10           15
Arg Gly Leu Glu Val Asn Lys Cys Glu Ile Ala Arg Phe Tyr Lys Leu
    20           25           30
His Glu Arg Arg Cys Glu Pro Ile Ala Met Thr Val Pro Arg Lys Ser
    35           40           45
Asp Leu Phe Gln Glu Asp Leu Tyr Pro Pro Thr Ala Gly Pro Asp Pro
    50           55           60
Ala Leu Thr Ala Glu Glu Trp Leu Gly Gly Arg Asp Ala Gly Pro Leu
65           70           75           80
Leu Ile Ser Leu Lys Asp Gly Tyr Val Pro Pro Lys Ser Arg Glu Leu
    85           90           95
Arg Val Asn Arg Gly Leu Asp Thr Gly Arg Arg Arg Ala Ala Pro Glu
    100          105          110
Ala Ser Gly Thr Pro Ser Ser Asp Ala Val Ser Arg Leu Glu Glu Glu
    115          120          125
Met Arg Lys Leu Gln Ala Thr Val Gln Glu Leu Gln Lys Arg Leu Asp
    130          135          140
Arg Leu Glu Glu Thr Val Gln Ala Lys
145           150

```

FIG.10M

57/66

```

atgggctaca tgcccaaacg tggcctggag gtgaacaagt gtgagatcgc caggttctac 60
aagctgcacg agcggaggtg tgagccatt gccatgacag tgcctcgaaa gtcggacctg 120
ttccaggagg acctgtaccc acccaccgca gggcccgacc ctgccctcac ggctgaggag 180
tggctggggg gtcgggatgc tgggccctc ctcattctcc tcaaggatgg ctacgtaccc 240
ccaaagagcc gggagctgag ggtcaaccgg ggcctggaca ccgggcgcag gagggcagca 300
ccagaggcca gtggcactcc cagctcggat gccgtgtctc ggctggagga ggagatgcgg 360
aagctccagg ccacggtgca ggagctccag aagcgcttgg acaggctgga ggagacagtc 420
caggccaagt ag 432

```

```

Met Gly Tyr Met Pro Lys Arg Gly Leu Glu Val Asn Lys Cys Glu Ile
 1           5           10           15
Ala Arg Phe Tyr Lys Leu His Glu Arg Arg Cys Glu Pro Ile Ala Met
      20           25           30
Thr Val Pro Arg Lys Ser Asp Leu Phe Gln Glu Asp Leu Tyr Pro Pro
      35           40           45
Thr Ala Gly Pro Asp Pro Ala Leu Thr Ala Glu Glu Trp Leu Gly Gly
      50           55           60
Arg Asp Ala Gly Pro Leu Leu Ile Ser Leu Lys Asp Gly Tyr Val Pro
65           70           75           80
Pro Lys Ser Arg Glu Leu Arg Val Asn Arg Gly Leu Asp Thr Gly Arg
      85           90           95
Arg Arg Ala Ala Pro Glu Ala Ser Gly Thr Pro Ser Ser Asp Ala Val
      100          105          110
Ser Arg Leu Glu Glu Glu Met Arg Lys Leu Gln Ala Thr Val Gln Glu
      115          120          125
Leu Gln Lys Arg Leu Asp Arg Leu Glu Glu Thr Val Gln Ala Lys
      130          135          140

```

FIG.10N

58/66

```

atgcccaaac gtggcctgga ggtgaacaag tgtgagatcg ccaggttcta caagctgcac   60
gagcggaggt gtgagcccat tgccatgaca gtgcctcgaa agtcggacct gttccaggag  120
gacctgtacc caccacccgc agggcccgcac cctgccctca cggctgagga gtggctgggg  180
ggtcgggatg ctgggcccct cctcatctcc ctcaaggatg gctacgtacc ccaaagagc   240
cgggagctga gggtaaccg gggcctggac accgggcgca ggagggcagc accagaggcc  300
agtggcactc ccagctcgga tgccgtgtct cggctggagg aggagatgcg gaagctccag  360
gccacggtgc aggagctcca gaagcgcttg gacaggctgg aggagacagt ccaggccaag  420
tag

```

```

Met Pro Lys Arg Gly Leu Glu Val Asn Lys Cys Glu Ile Ala Arg Phe
 1           5           10           15
Tyr Lys Leu His Glu Arg Arg Cys Glu Pro Ile Ala Met Thr Val Pro
      20           25           30
Arg Lys Ser Asp Leu Phe Gln Glu Asp Leu Tyr Pro Pro Thr Ala Gly
      35           40           45
Pro Asp Pro Ala Leu Thr Ala Glu Glu Trp Leu Gly Gly Arg Asp Ala
      50           55           60
Gly Pro Leu Leu Ile Ser Leu Lys Asp Gly Tyr Val Pro Pro Lys Ser
65           70           75           80
Arg Glu Leu Arg Val Asn Arg Gly Leu Asp Thr Gly Arg Arg Arg Ala
      85           90           95
Ala Pro Glu Ala Ser Gly Thr Pro Ser Ser Asp Ala Val Ser Arg Leu
      100          105          110
Glu Glu Glu Met Arg Lys Leu Gln Ala Thr Val Gln Glu Leu Gln Lys
      115          120          125
Arg Leu Asp Arg Leu Glu Glu Thr Val Gln Ala Lys
      130          135          140

```

FIG.100

59/66

```

atgacagtgc ctcgaaagtc ggacctgttc caggaggacc tgtaccacc caccgcaggg 60
cccgaccctg ccctcacggc tgaggagtgg ctgggggggtc gggatgctgg gcccctcctc 120
atctccctca aggatggcta cgtaccccca aagagccggg agctgagggt caaccggggc 180
ctggacaccg ggcgcaggag ggcagcacca gaggccagtg gcactcccag ctcggatgcc 240
gtgtctcggc tggaggagga gatgcggaag ctccaggcca cggtcagga gctccagaag 300
cgcttgaca ggctggagga gacagtccag gccaagtag 339

```

```

Met Thr Val Pro Arg Lys Ser Asp Leu Phe Gln Glu Asp Leu Tyr Pro
 1           5           10           15
Pro Thr Ala Gly Pro Asp Pro Ala Leu Thr Ala Glu Glu Trp Leu Gly
      20           25           30
Gly Arg Asp Ala Gly Pro Leu Leu Ile Ser Leu Lys Asp Gly Tyr Val
      35           40           45
Pro Pro Lys Ser Arg Glu Leu Arg Val Asn Arg Gly Leu Asp Thr Gly
      50           55           60
Arg Arg Arg Ala Ala Pro Glu Ala Ser Gly Thr Pro Ser Ser Asp Ala
65           70           75           80
Val Ser Arg Leu Glu Glu Met Arg Lys Leu Gln Ala Thr Val Gln
      85           90           95
Glu Leu Gln Lys Arg Leu Asp Arg Leu Glu Glu Thr Val Gln Ala Lys
      100           105           110

```

FIG.10P

```

atgctgggcc cctcctcatc tccctcaagg atggctacgt acccccaaag agccgggagc 60
tga 63

```

```

Met Leu Gly Pro Ser Ser Ser Pro Ser Arg Met Ala Thr Tyr Pro Gln
 1           5           10           15
Arg Ala Gly Ser
      20

```

FIG.10Q

```

atggctacgt acccccaaag agccgggagc tga 33

```

```

Met Ala Thr Tyr Pro Gln Arg Ala Gly Ser
 1           5           10

```

FIG.10R

60/66

atgccgtgtc tcggctggag gaggagatgc ggaagctcca ggccacggtg caggagctcc 60  
 agaagcgctt ggacaggctg gaggagacag tccaggccaa gtagagcccc gcagggcctc 120  
 cagcagggtc agccattcac acccatccac tcacctcca ttcccagcca catggcagag 180  
 aaaaaaatca taataaaatg gctttatatt ctggtaaaaa aaaaaaaaaa ggcgggcc 238

Met Pro Cys Leu Gly Trp Arg Arg Arg Cys Gly Ser Ser Arg Pro Arg  
 1 5 10 15  
 Cys Arg Ser Ser Arg Ser Ala Trp Thr Gly Trp Arg Arg Gln Ser Arg  
 20 25 30  
 Pro Ser Arg Ala Pro Gln Gly Leu Gln Gln Gly Gln Pro Phe Thr Pro  
 35 40 45  
 Ile His Ser Pro Pro Ile Pro Ser His Met Ala Glu Lys Lys Ile Ile  
 50 55 60  
 Ile Lys Trp Leu Tyr Phe Leu Val Lys Lys Lys Lys Lys Gly Gly  
 65 70 75

FIG. 10S

atgcggaagc tccaggccac ggtgcaggag ctccagaagc gcttggacag gctggaggag 60  
 acagtccagg ccaagtag 78

Met Arg Lys Leu Gln Ala Thr Val Gln Glu Leu Gln Lys Arg Leu Asp  
 1 5 10 15  
 Arg Leu Glu Glu Thr Val Gln Ala Lys  
 20 25

FIG. 10T

atggcagaga aaaaaatcat aataaaatgg ctttatatttc tggtaaaaaa aaaaaaaag 60  
 ggcgggcc

Met Ala Glu Lys Lys Ile Ile Ile Lys Trp Leu Tyr Phe Leu Val Lys  
 1 5 10 15  
 Lys Lys Lys Lys Gly Gly  
 20

FIG. 10U

atggctttat tttctggtaa aaaaaaaaaa aaagggcggc c 41

Met Ala Leu Phe Ser Gly Lys Lys Lys Lys Lys Gly Arg  
 1 5 10

FIG. 10V

61/66

```

atgttcgcct ggcceaagct cgcctgcacc ccctctctga tccgagctgg atccagagtt 60
gcatacagac caatttctgc atcagtgtta tctcgaccag aggctagtag gactggagag 120
ggctctacgg tatttaatgg ggcccagaat ggtgtgtctc agctaatacca aaggagagttt 180
cagaccagtg caatcagcag agacattgat actgctgcca aatttattgg tgcaggtgct 240
gcaacagtag gagtggctgg ttctgggtgct ggtattggaa cagtctttgg cagccttatc 300
attggttatg ccagaaaccc ttcgctgaag cagcagctgt tctcatatgc tatcctggga 360
tttgccttgt ctgaagctat gggctctctt tgtttgatgg ttgctttctt gattttgttt 420
gccatgtaa 429

```

```

Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser Leu Ile Arg Ala
 1           5           10          15
Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser Val Leu Ser Arg
          20          25          30
Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val Phe Asn Gly Ala
          35          40          45
Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe Gln Thr Ser Ala
          50          55          60
Ile Ser Arg Asp Ile Asp Thr Ala Ala Lys Phe Ile Gly Ala Gly Ala
65          70          75          80
Ala Thr Val Gly Val Ala Gly Ser Gly Ala Gly Ile Gly Thr Val Phe
          85          90          95
Gly Ser Leu Ile Ile Gly Tyr Ala Arg Asn Pro Ser Leu Lys Gln Gln
          100          105          110
Leu Phe Ser Tyr Ala Ile Leu Gly Phe Ala Leu Ser Glu Ala Met Gly
          115          120          125
Leu Phe Cys Leu Met Val Ala Phe Leu Ile Leu Phe Ala Met
          130          135          140

```

FIG.11A

```

atggggccca gaatggtgtg tctcagctaa 30

```

```

Met Gly Pro Arg Met Val Cys Leu Ser
 1           5

```

FIG.11B

```

atggtgtgtc tcagctaa 18

```

```

Met Val Cys Leu Ser
 1           5

```

FIG.11C

62/66

atgccagaaa cccttcgctg a 21

Met Pro Glu Thr Leu Arg  
 1 5

FIG.11D

atgctatcct gggatttgcc ttgtctgaag ctatgggtct cttttgtttg a 51

Met Leu Ser Trp Asp Leu Pro Cys Leu Lys Leu Trp Val Ser Phe Val  
 1 5 10 15

FIG.11E

atgggtctct tttgtttgat ggttgctttc ttgattttgt ttgccatgta a 51

Met Gly Leu Phe Cys Leu Met Val Ala Phe Leu Ile Leu Phe Ala Met  
 1 5 10 15

FIG.11F

atggttgctt tcttgatttt gtttgccatg taa 33

Met Val Ala Phe Leu Ile Leu Phe Ala Met  
 1 5 10

FIG.11G

atgttggcat tcatattaat tacggatgta attctgtgta tcttactgtg a 51

Met Leu Ala Phe Ile Leu Ile Thr Asp Val Ile Leu Cys Ile Leu Leu  
 1 5 10 15

FIG.11H

atgggaatgt acgttatttc caaagtcatt tcattaaaga tgaaaacttt aaaaaaaaaa 60  
 aaaaaagggc ggcc 74

Met Gly Met Tyr Val Ile Ser Lys Val Ile Ser Leu Lys Met Lys Thr  
 1 5 10 15  
 Leu Lys Lys Lys Lys Lys Gly Arg  
 20

FIG.11I

63/66

atgaagacag agccccaccc tcagatgcac atgagctggc gggattga 48

Met	Lys	Thr	Glu	Pro	His	Pro	Gln	Met	His	Met	Ser	Trp	Arg	Asp
1				5				10						15

FIG.12A

atgcacatga gctggcggga ttga 24

Met	His	Met	Ser	Trp	Arg	Asp
1				5		

FIG.12B

atgagctggc gggattga 18

Met	Ser	Trp	Arg	Asp
1				5

FIG.12C

atgctgtctt	cgtactggga	aagggatit	cagccctcag	aatcgctcca	ccttgcagct	60
ctcccccttct	ctgtattcct	agaaactgac	acatgctga			99

Met	Leu	Ser	Ser	Tyr	Trp	Glu	Arg	Asp	Phe	Gln	Pro	Ser	Glu	Ser	Leu
1				5					10					15	
His	Leu	Ala	Ala	Leu	Pro	Phe	Ser	Val	Phe	Leu	Glu	Thr	Asp	Thr	Cys
		20						25					30		

FIG.12D

atgctgaaca	tcacagctta	tttcctcatt	tttataatgt	cccttcacaa	accagtggt	60
ttaggagcat	ga					72

Met	Leu	Asn	Ile	Thr	Ala	Tyr	Phe	Leu	Ile	Phe	Ile	Met	Ser	Leu	His
1				5				10						15	
Lys	Pro	Ser	Val	Leu	Gly	Ala									
				20											

FIG.12E



64/66

atgtcccttc acaaaccag tgttttagga gcatga 36

Met	Ser	Leu	His	Lys	Pro	Ser	Val	Leu	Gly	Ala
1				5				10		

FIG.12F

atgagtgccg	tgtgtgtgcg	tcctgtcgga	gccctgtctc	ctctctctgt	aataaactca	60
tttctagcag	aaaaaaaaa	aaaaaaaaa	gggcggcc			98

Met	Ser	Ala	Val	Cys	Val	Arg	Pro	Val	Gly	Ala	Leu	Ser	Pro	Leu	Ser
1				5					10					15	
Val	Ile	Asn	Ser	Phe	Leu	Ala	Glu	Lys	Lys	Lys	Lys	Lys	Lys	Gly	Arg
				20				25					30		

FIG.12G

65/66

atgcaagcat ccccggtcca gtga 24

Met Gln Ala Ser Pro Phe Gln

1

5

FIG.13A

atgcagctca aaacgcttag cctagccaca ccccccacggg aaacagcagt gattaacctt 60  
tag 63

Met Gln Leu Lys Thr Leu Ser Leu Ala Thr Pro Pro Arg Glu Thr Ala

1

5

10

15

Val Ile Asn Leu

20

FIG.13B

atgcttagcc ctaaacctca acagttaaact caacaaaact gctcgccaga acactacgag 60  
ccacagctta aaactcaaag gacctggcgg tgcttcatac ccctctag 108

Met Leu Ser Pro Lys Pro Gln Gln Leu Asn Gln Gln Asn Cys Ser Pro

1

5

10

15

Glu His Tyr Glu Pro Gln Leu Lys Thr Gln Arg Thr Trp Arg Cys Phe

20

25

30

Ile Pro Leu

35

FIG.13C

atgaaggcta caaagtaa 18

Met Lys Ala Thr Lys

1

5

FIG.13D

atgggggtggc aagaaatggg ctacattttc taccccagaa aactacgata g 51

Met Gly Trp Gln Glu Met Gly Tyr Ile Phe Tyr Pro Arg Lys Leu Arg

1

5

10

15

FIG.13E

66/66

atgggctaca ttttctaccc cagaaaacta cgatag 36

Met Gly Tyr Ile Phe Tyr Pro Arg Lys Leu Arg  
 1 5 10

FIG.13F

atgaaactta agggtcgaag gtggatttag 30

Met Lys Leu Lys Gly Arg Arg Trp Ile  
 1 5

FIG.13G

atggttaagtg tactggaaag tgcacttgga cgaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 120  
 aaaaaaaaaa aaaaaaaaaa aaaagggcgg cc 152

Met Val Ser Val Leu Glu Ser Ala Leu Gly Arg Lys Lys Lys Lys Lys  
 1 5 10 15  
 Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys  
 20 25 30  
 Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys  
 35 40 45  
 Gly Arg  
 50

FIG.13H

## SEQUENCE LISTING

<110> Shawn Barney  
Mary Beth Thomas  
Stuart D. Portbury  
Kasturi Puranam  
Lawrence C. Katz  
Donald C. Lo

<120> COMPOSITIONS AND METHODS FOR DIAGNOSING  
AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
CELL DEATH

<130> 10001-0006-999

<160> 342

<170> FastSEQ for Windows Version 4.0

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<211> 1794  
<212> DNA  
<213> Homo Sapiens

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agaaaatagt aaaaaaatat tttaatgata taaaatcctt ggctgctagc taggagtcgc 180  
tctgtgctat agtagaaaaa tatggagact gggagctgtg tgatctatct tcaccagtaa 240  
ctgggtgact ttaaaaggcc tgtaacttgt acttgtctac ttttatccag ttctacactg 300  
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attcagaaca ttgccattta aggaatggca aagatttttt cccataagtt aaaagatcaa 420  
atatgaaatt aatataagtt ataaagtata tatttcttca acaataatgt acagttgaag 480  
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ttctgagggc tgcgaaggca ggatatgttc caggcctccc tctatggctt gtagatggcc 720  
atcttcatgg tcacatggca ttctccctgt agctctctgt ttccagactt cccctttttg 780  
taaggatata agtgatatta gattagggtc ttccctaagg acctcatttg acctgcctgg 840  
gctcaagcta ttctccacc tctgcctccc taagagctgg gattacaggc atgagccatc 900  
acaccgccc ctcattttaa tttgattacc tctgtaaata cctctgtctc caaatgagat 960  
ttcatcctga gcagctgggg gttaggactt caatatatga atttgacagg gagggtagaa 1020  
ggagagaaca gaattcaacc cacagcagca acaatctaag agcttctgtg gagcaagcaa 1080  
agagaatggt cattgtcagt ctcataggcg ccattcccta ttcatagctt acttggtgctc 1140  
tctcatattc cttgagtgtt ttaaattgta aacattcaag tacaacaaa cttcgcttga 1200  
ttaccagaga taaaaaagaa atgccttgta atttgggtgc atgtgaatgt ttttaagtga 1260  
tacctgaaaa attgtactta agaatggcat aagagctttc tgattttcat tttacttcca 1320  
ttaaagggga aaatatgcat agactgtcta tccattagcc agaacaatgg gacctctccc 1380  
atcttaaaat aaaagccaaa ataactctggc caccaggaag aaagggtaga gcttggaat 1440  
gtcctcagga gattgtaaag atgcgtttcc ttgattcttt tgcctcact cttccctgtg 1500  
actatttcct ccttcagggc tctatttctg ggttgggaga atgctgttcc agcaccaagc 1560  
agtgtgggta tatatatcca taccaaagag gcaatttgat tgccttgga gttacaaaaa 1620  
accaaagtgc aatgcctgat tagggaatac aacaataaaa gtaaaaaataa tttaggagta 1680  
tatatgcaga acatcagcct ttaaagtaat cttttattag gaaaatggca ttcacgattt 1740  
gagaagatgg aagggtgtgg ggaacagaaa taaaaaaaaa aaaaaagggc ggcc 1794

<210> 2  
<211> 39  
<212> DNA  
<213> Homo Sapiens

<400> 2  
atggagactg ggagctgtgt gatctatctt caccagtaa

39

<210> 3  
<211> 12  
<212> PRT  
<213> Homo Sapiens

<400> 3  
Met Glu Thr Gly Ser Cys Val Ile Tyr Phe His Gln  
1 5 10

<210> 4  
<211> 45  
<212> DNA  
<213> Homo Sapiens

<400> 4  
atgattctca acatcttttt ctggtatgta agactttcct catga 45

<210> 5  
<211> 14  
<212> PRT  
<213> Homo Sapiens

<400> 5  
Met Ile Leu Asn Ile Phe Phe Trp Tyr Val Arg Leu Ser Ser  
1 5 10

<210> 6  
<211> 51  
<212> DNA  
<213> Homo Sapiens

<400> 6  
atgaaattca gaacattgcc atttaaggaa tggcaaagat tttttcccta a 51

<210> 7  
<211> 16  
<212> PRT  
<213> Homo Sapiens

<400> 7  
Met Lys Phe Arg Thr Leu Pro Phe Lys Glu Trp Gln Arg Phe Phe Pro  
1 5 10 15

<210> 8  
<211> 42  
<212> DNA  
<213> Homo Sapiens

<400> 8  
atggcaaaga ttttttcct aaagttaaaa gatcaaatat ga 42

<210> 9  
<211> 13  
<212> PRT  
<213> Homo Sapiens

<400> 9  
Met Ala Lys Ile Phe Ser Leu Lys Leu Lys Asp Gln Ile  
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Arg Leu Gly Ser Ser Leu Arg Thr Ser Phe Asp Leu Pro Gly Leu Lys

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Leu Phe Ser His Leu Cys Leu Pro Lys Ser Trp Asp Tyr Arg His Glu

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Pro Asp Phe Pro Phe Leu

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<213> Homo Sapiens

<400> 100  
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<210> 101  
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<400> 101  
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Leu Phe Asn Asp  
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<210> 102  
<211> 42  
<212> DNA  
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<400> 102  
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<210> 103  
<211> 13  
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<213> Homo Sapiens

<400> 103  
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1 5 10

<210> 104

<211> 116  
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<400> 104  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaagg gcggcc 116

<210> 105  
 <211> 38  
 <212> PRT  
 <213> Homo Sapiens

<400> 105  
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 20 25 30  
 Lys Lys Lys Lys Gly Arg  
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<210> 106  
 <211> 2144  
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<400> 106  
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 tagctggggg ctagaagatg acgaagacat gacacttaca agatggacag ggatgataat 180  
 tgggcctcca agaacaattt atgaaaaccg aatatacagc cttaaaatag aatgtggacc 240  
 taaataccca gaagcacccc cctttgtaag atttgtaaca aaaattaata tgaatggagt 300  
 aaatagttct aatggagtgg tggacccaag agccatatca gtgctagcaa aatggcagaa 360  
 ttcatatagc atcaaagtgt tcctgcaaga gcttcggcgc ctaatgatgt ctaaagaaaa 420  
 tatgaaactc cctcagcgc ccgaaggaca gtgttacagc aattaatcaa aaagaaaaac 480  
 cacaggccct tccccttccc cccaattcga ttaatcagt cttcattttc cacagtagta 540  
 aattttctag atacgtcttg tagacctcaa agtaccggaa aggaagctcc cattcaaagg 600  
 aaatttatct taagatactg taaatgatac taattttttc gtccatttga aatatataag 660  
 ttgtgtctata acaaatcatc ctgtcaagtgt taaccactgt ccacgtagtt gaacttcttg 720  
 gatcaagaaa gtctatttaa attgattccc atcataactg gtggggcaca tctaactcaa 780  
 ctgtgaaaag cacatcacca caatcacctt gctgctgatt acacggcctg gggctctctg 840  
 cttctcccct taccctccc cctcccaccc tccttgcaac aacagccctc tagcctgggg 900  
 ggcttggttag agtagatgtg aaggtttcag gtcgcagcct gtgggactac tgctaggtgt 960  
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 cttgttaagca cacatgatcc ctctgaattg ttttactttc ctgtaactgc ttttgctttt 1560  
 aaaaattgaa gaagttttta acagggtctt catttggtca tccttgcaat ccattggggg 1620  
 ctagtttggg atctgacaac tggaaacaaa agaacttga atccggtgca tgccttgggt 1680  
 ttggtgctgc tgctgcttcc caagatcctc agcagggtat aagaaggaaac ccggtgtgca 1740  
 cagcagatcc ccgaaattgg tgggcttgac ctcttggaat attgctgctg ctttccactc 1800  
 gctgttcagg accactaaat gctgaaatgt ggtgcatcac cgaaataaaa gcaattcatt 1860  
 gtgtactaaa gggttttttt ttttttttaa tttagtattt gtgtaaaaac accttttgaa 1920  
 gcagcaacta tcaagtctga aaagcaattg atgtttccat taatcttttt ctgggggggaa 1980  
 aaccttagtt ctaaggattt aacatcctgt aagtgaagt taacataaca gtattccata 2040  
 agcagccttt ttattgtcag accattgcct gattttaata taataaaaaa aaagtgtgcg 2100  
 ttaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc ggcc 2144

<210> 107

18/60

<211> 444  
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 gaagacatga cacttacaag atggacaggg atgataattg ggcctccaag aacaatttat 180  
 gaaaaccgaa tatacagcct taaaatagaa tgtggaccta aatacccaga agcaccctccc 240  
 tttgtaagat ttgtaacaaa aattaatatg aatggagtaa atagttctaa tggagtgggtg 300  
 gacccaagag ccatatcagt gctagcaaaa tggcagaatt catatagcat caaagttgtc 360  
 ctgcaagagc ttcggcgctt aatgatgtct aaagaaaata tgaaactccc tcagccgccc 420  
 gaaggacagt gttacagcaa ttaa 444

<210> 108  
 <211> 147  
 <212> PRT  
 <213> Homo Sapiens

<400> 108  
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 20 25 30  
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 35 40 45  
 Thr Gly Met Ile Ile Gly Pro Arg Thr Ile Tyr Glu Asn Arg Ile  
 50 55 60  
 Tyr Ser Leu Lys Ile Glu Cys Gly Pro Lys Tyr Pro Glu Ala Pro Pro  
 65 70 75 80  
 Phe Val Arg Phe Val Thr Lys Ile Asn Met Asn Gly Val Asn Ser Ser  
 85 90 95  
 Asn Gly Val Val Asp Pro Arg Ala Ile Ser Val Leu Ala Lys Trp Gln  
 100 105 110  
 Asn Ser Tyr Ser Ile Lys Val Val Leu Gln Glu Leu Arg Arg Leu Met  
 115 120 125  
 Met Ser Lys Glu Asn Met Lys Leu Pro Gln Pro Pro Glu Gly Gln Cys  
 130 135 140  
 Tyr Ser Asn  
 145

<210> 109  
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 <212> DNA  
 <213> Homo Sapiens

<400> 109  
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<210> 110  
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 <212> PRT  
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<400> 110  
 Met Ala Gln Leu Ala Gly Val  
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<210> 111  
 <211> 15  
 <212> DNA  
 <213> Homo Sapiens

<400> 111  
 atgacgaaga catga 15

19/60

<210> 112  
 <211> 4  
 <212> PRT  
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<400> 112  
 Met Thr Lys Thr  
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<210> 113  
 <211> 318  
 <212> DNA  
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<400> 113  
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 agatttgtaa caaaaattaa tatgaatgga gtaaatagtt ctaatggagt ggtggaccca 180  
 agagccatat cagtgcctagc aaaatggcag aattcatata gcatcaaagt tgtcctgcaa 240  
 gagcttcggc gcctaataat gtctaaagaa aatatgaaac tccctcagcc gcccgaagga 300  
 cagtgttaca gcaattaa 318

<210> 114  
 <211> 105  
 <212> PRT  
 <213> Homo Sapiens

<400> 114  
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 Ile Tyr Glu Asn Arg Ile Tyr Ser Leu Lys Ile Glu Cys Gly Pro Lys  
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 Tyr Pro Glu Ala Pro Pro Phe Val Arg Phe Val Thr Lys Ile Asn Met  
 35 40 45  
 Asn Gly Val Asn Ser Ser Asn Gly Val Val Asp Pro Arg Ala Ile Ser  
 50 55 60  
 Val Leu Ala Lys Trp Gln Asn Ser Tyr Ser Ile Lys Val Val Leu Gln  
 65 70 75 80  
 Glu Leu Arg Arg Leu Met Met Ser Lys Glu Asn Met Lys Leu Pro Gln  
 85 90 95  
 Pro Pro Glu Gly Gln Cys Tyr Ser Asn  
 100 105

<210> 115  
 <211> 42  
 <212> DNA  
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<400> 115  
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<210> 116  
 <211> 13  
 <212> PRT  
 <213> Homo Sapiens

<400> 116  
 Met Asp Arg Asp Asp Asn Trp Ala Ser Lys Asn Asn Leu  
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<210> 117  
 <211> 294  
 <212> DNA  
 <213> Homo Sapiens

<400> 117  
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 aatggagtaa atagttctaa tggagtgggtg gacccaagag ccatatcagt gctagcaaaa 180  
 tggcagaatt catatagcat caaagttgtc ctgcaagagc ttcggcgct aatgatgtct 240  
 aaagaaaata tgaaactccc tcagccgccc gaaggacagt gttacagcaa ttaa 294

<210> 118  
 <211> 97  
 <212> PRT  
 <213> Homo Sapiens

<400> 118  
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 1 5 10 15  
 Leu Lys Ile Glu Cys Gly Pro Lys Tyr Pro Glu Ala Pro Pro Phe Val  
 20 25 30  
 Arg Phe Val Thr Lys Ile Asn Met Asn Gly Val Asn Ser Ser Asn Gly  
 35 40 45  
 Val Val Asp Pro Arg Ala Ile Ser Val Leu Ala Lys Trp Gln Asn Ser  
 50 55 60  
 Tyr Ser Ile Lys Val Val Leu Gln Glu Leu Arg Arg Leu Met Met Ser  
 65 70 75 80  
 Lys Glu Asn Met Lys Leu Pro Gln Pro Pro Glu Gly Gln Cys Tyr Ser  
 85 90 95  
 Asn

<210> 119  
 <211> 30  
 <212> DNA  
 <213> Homo Sapiens

<400> 119  
 atgaaaaccg aatatacagc cttaaaatag 30

<210> 120  
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 <212> PRT  
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<400> 120  
 Met Lys Thr Glu Tyr Thr Ala Leu Lys  
 1 5

<210> 121  
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<400> 121  
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<210> 122  
 <211> 3  
 <212> PRT  
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<400> 122  
 Met Trp Thr  
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<210> 123  
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 <212> DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 123

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atgaatggag taaatagttc taatggagtg gtggacccaa gagccatatc agtgctagca      60
aaatggcaga attcatatag catcaaagtt gtcctgcaag agcttcggcg cctaataatg      120
tctaaagaaa atatgaaact ccctcagccg cccgaaggac agtggttacag caattaa      177

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&lt;210&gt; 124

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 124

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Met Asn Gly Val Asn Ser Ser Asn Gly Val Val Asp Pro Arg Ala Ile
  1              5              10              15
Ser Val Leu Ala Lys Trp Gln Asn Ser Tyr Ser Ile Lys Val Val Leu
              20              25              30
Gln Glu Leu Arg Arg Leu Met Met Ser Lys Glu Asn Met Lys Leu Pro
      35              40              45
Gln Pro Pro Glu Gly Gln Cys Tyr Ser Asn
      50              55

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&lt;210&gt; 125

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 125

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atggagtggt ggacccaaga gccatatcag tgctag      36

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&lt;210&gt; 126

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 126

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Met Glu Trp Trp Thr Gln Glu Pro Tyr Gln Cys
  1              5              10

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&lt;210&gt; 127

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 127

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atggcagaat tcatatag      18

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&lt;210&gt; 128

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 128

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Met Ala Glu Phe Ile
  1              5

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&lt;210&gt; 129

&lt;211&gt; 63

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 129

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atgatgtcta aagaaaatat gaaactccct cagccgcccc aaggacagtg ttacagcaat      60
taa      63

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<210> 130  
<211> 20  
<212> PRT  
<213> Homo Sapiens

<400> 130  
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1 5 10 15  
Cys Tyr Ser Asn  
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<210> 131  
<211> 60  
<212> DNA  
<213> Homo Sapiens

<400> 131  
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<210> 132  
<211> 19  
<212> PRT  
<213> Homo Sapiens

<400> 132  
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1 5 10 15  
Tyr Ser Asn

<210> 133  
<211> 45  
<212> DNA  
<213> Homo Sapiens

<400> 133  
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<210> 134  
<211> 14  
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<213> Homo Sapiens

<400> 134  
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1 5 10

<210> 135  
<211> 27  
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<400> 135  
atgatactaa ttttttcgtc catttga 27

<210> 136  
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<212> PRT  
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<400> 136  
Met Ile Leu Ile Phe Ser Ser Ile  
1 5

<210> 137

<211> 72  
<212> DNA  
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<400> 137  
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catagattgt aa 72

<210> 138  
<211> 23  
<212> PRT  
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<400> 138  
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1 5 10 15  
Pro Trp Pro Lys His Arg Leu  
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<210> 139  
<211> 57  
<212> DNA  
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<210> 140  
<211> 18  
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1 5 10 15  
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<210> 141  
<211> 48  
<212> DNA  
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<400> 141  
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<210> 142  
<211> 15  
<212> PRT  
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<400> 142  
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<210> 143  
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<400> 143  
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<210> 144  
<211> 4

<212> PRT  
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<400> 144  
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<210> 145  
<211> 78  
<212> DNA  
<213> Homo Sapiens

<400> 145  
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tttgctttta aaaattga 78

<210> 146  
<211> 25  
<212> PRT  
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<400> 146  
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1 5 10 15  
Pro Val Thr Ala Phe Ala Phe Lys Asn  
20 25

<210> 147  
<211> 33  
<212> DNA  
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<400> 147  
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<210> 148  
<211> 10  
<212> PRT  
<213> Homo Sapiens

<400> 148  
Met Ile Pro Leu Asn Cys Phe Thr Phe Leu  
1 5 10

<210> 149  
<211> 156  
<212> DNA  
<213> Homo Sapiens

<400> 149  
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cccggtgtgc acagcagatc cccgaaattg gtgggcttga cctcctggca aattgctgctg 120  
tctttccact tgctgttcag gaccactaaa tgctga 156

<210> 150  
<211> 51  
<212> PRT  
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<400> 150  
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Ile Lys Lys Glu Pro Gly Val His Ser Arg Ser Pro Lys Leu Val Gly  
20 25 30  
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35 40 45  
 Thr Lys Cys  
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 <211> 30  
 <212> DNA  
 <213> Homo Sapiens  
 <400> 151  
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 <210> 152  
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 <212> PRT  
 <213> Homo Sapiens  
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 <210> 153  
 <211> 69  
 <212> DNA  
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 <400> 153  
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 tag 63  
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 <211> 20  
 <212> PRT  
 <213> Homo Sapiens  
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 Phe Phe Leu Ile  
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 <210> 157  
 <211> 66  
 <212> DNA  
 <213> Homo Sapiens

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 aagtga 66

<210> 158  
 <211> 21  
 <212> PRT  
 <213> Homo Sapiens

<400> 158  
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 1 5 10 15  
 Leu Thr Ser Cys Lys  
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<210> 159  
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 <212> DNA  
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 agccgagatc acaccactgc actccagcct gggtgacaag aacgaaactc catctcaaaa 120  
 aataaaataa aatatatact atcttgctcc tcagaaccag tggggaagaa gagggaaggc 180  
 aaagaaagaa actgagcata gtaaacacag catttttttg taggctctta tttaaaatgt 240  
 gtgtgtgtgt gtgtatgtgt gtgtttctga gtaagtattg actgggaaaa agagagaagt 300  
 caatcaaaag tatactgtgc aattgagaga ggctggccca agatttaaaa cttcctgtgg 360  
 gtaatctaac tgtgagtaga taggaatcgg ccatatgacg aaatgagatc aataggaaat 420  
 gtgctttttg aggaaatttt attttagtac caaatgttgc cagtgacaat cttcagttaa 480  
 gaagtaagtt atttgaccta aaattcttat ctctgccact ttggttttaa aacaaaaacc 540  
 cttatataca tggaatagtt atattttaat taagcattta ttttagttgt tttcatccat 600  
 tcaagcaaaa tgaataagca gcatttttca ttgcacttaa aaatgtaaaa tacctgcatg 660  
 ccactaatct gtaacatttt accagttcag atgcctgtaa tgtgtgactt tatgtgtgtc 720  
 tgtgtgtgtt tgaagagaat aaaggaaata atactttgca aactgtttta acaagtgttt 780  
 aaacttctat tggcaacatt tattgggcta agcagttatt gaaaactccg catagtttta 840  
 ttttccattt gaaacttcaa tcaaatacaag actattatat tcattaggga attaaagact 900  
 aatttgcttt ttaaattgtga agtggaacac tgtgtggaat gtaaatgtgt gatgaagcaa 960  
 aatgtataaa gtatgaaata ttatactttt accctggata attattcagg accccagttg 1020  
 gcccaaatag gtgcaatttt taatcctttg aaattagcca gccagacctt atgctaagggt 1080  
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 ttctgtcagg aatgatattt ccaaatgaaa atgtaaagaa cattgggaaa taataaactt 1200  
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<210> 160  
 <211> 45  
 <212> DNA  
 <213> Homo Sapiens

<400> 160  
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<210> 161  
 <211> 14  
 <212> PRT  
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<400> 161  
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<210> 162  
 <211> 27  
 <212> DNA  
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<400> 162  
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<210> 163  
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<212> PRT  
<213> Homo Sapiens

<400> 163  
Met Cys Val Phe Leu Ser Lys Tyr  
1 5

<210> 164  
<211> 12  
<212> DNA  
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<400> 164  
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<210> 165  
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<400> 165  
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<210> 166  
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<210> 167  
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<400> 167  
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1 5 10

<210> 168  
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 1 5  
  
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 35 40 45  
 Ile Gly Leu Ser Ser Tyr  
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 <400> 176  
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29/60

agcagttatt ga

132

&lt;210&gt; 177

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 177

Met	Pro	Val	Met	Cys	Asp	Phe	Met	Cys	Val	Cys	Val	Val	Leu	Lys	Arg
1				5					10					15	
Ile	Lys	Glu	Ile	Ile	Leu	Cys	Lys	Leu	Phe	Lys	Gln	Val	Phe	Lys	Leu
			20					25					30		
Leu	Leu	Ala	Thr	Phe	Ile	Gly	Leu	Ser	Ser	Tyr					
		35					40								

&lt;210&gt; 178

&lt;211&gt; 123

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 178

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aaactgttta	aacaagtgtt	taaacttcta	ttggcaacat	ttattgggct	aagcagttat	120
tga						123

&lt;210&gt; 179

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 179

Met	Cys	Asp	Phe	Met	Cys	Val	Cys	Val	Val	Leu	Lys	Arg	Ile	Lys	Glu
1				5					10					15	
Ile	Ile	Leu	Cys	Lys	Leu	Phe	Lys	Gln	Val	Phe	Lys	Leu	Leu	Leu	Ala
			20					25					30		
Thr	Phe	Ile	Gly	Leu	Ser	Ser	Tyr								
		35					40								

&lt;210&gt; 180

&lt;211&gt; 111

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 180

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caagtgttta	aacttctatt	ggcaacattt	attgggctaa	gcagttattg	a	111

&lt;210&gt; 181

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 181

Met	Cys	Val	Cys	Val	Val	Leu	Lys	Arg	Ile	Lys	Glu	Ile	Ile	Leu	Cys
1				5					10					15	
Lys	Leu	Phe	Lys	Gln	Val	Phe	Lys	Leu	Leu	Leu	Ala	Thr	Phe	Ile	Gly
			20					25					30		
Leu	Ser	Ser	Tyr												
		35													

&lt;210&gt; 182

&lt;211&gt; 57

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens



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<211> 18  
<212> PRT  
<213> Homo Sapiens

<400> 183  
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Pro Gly

<210> 184  
<211> 18  
<212> DNA  
<213> Homo Sapiens

<400> 184  
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<210> 185  
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<400> 185  
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<210> 186  
<211> 15  
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<400> 186  
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<400> 187  
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<210> 188  
<211> 99  
<212> DNA  
<213> Homo Sapiens

<400> 188  
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gcaattttta atcctttgaa attagccagc cagacctaa 99

<210> 189  
<211> 32  
<212> PRT  
<213> Homo Sapiens

<400> 189  
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Ala Gln Ile Gly Ala Ile Phe Asn Pro Leu Lys Leu Ala Ser Gln Thr  
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<211> 12

<212> DNA

<213> Homo Sapiens

<400> 190

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<210> 191

<211> 3

<212> PRT

<213> Homo Sapiens

<400> 191

Met Leu Arg

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<210> 192

<211> 63

<212> DNA

<213> Homo Sapiens

<400> 192

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60

63

<210> 193

<211> 20

<212> PRT

<213> Homo Sapiens

<400> 193

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 Asn Ile Gly Lys  
                   20

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<211> 42

<212> DNA

<213> Homo Sapiens

<400> 194

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42

<210> 195

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 195

Met Ile Phe Pro Asn Glu Asn Val Lys Asn Ile Gly Lys  
   1                  5                  10

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<211> 12

<212> DNA

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<400> 196

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12

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 ttttgggtgt tagactgaaa tattttaaga gtatttaacc tttccagtat tctgtttcac 180  
 gcttagatgg aaatgtatct tatgaataga gacatattaa aataatgttt acatcttaga 240  
 aaaaacatag atagtgtctag taatattact tataactgta atatatagat tcagaaaatac 300  
 attttcatta tccaaaatca gcttcaacaa atgggttctg gagacaaata atttgttttc 360  
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 gacttgctaa tttcagaaat aattattcat ttttaaaaag ccccttttaa agcatctact 600  
 tgaagattgg tataattttc ataaaatgtc ttttttttta gtgtcccaaa gatattcttag 660  
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 agtttcatcc atggtgaatg gtacaaaata tttctgtgaa actaacagga agatattttc 780  
 agataactag gataacttgt tgctttgtta cccagcctaa ttgaagagtg gcagagacta 840  
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 gtcttttaca tgcttggttc aaagaaccaa cagaaaaaaa agctaagaaa actgagaact 960  
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 tattttttaga tgatgtaaca tagccatcaa aattaatatt atgtaatgcc taatacttag 1320  
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<400> 199  
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<400> 200  
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 35 40

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<211> 69  
<212> DNA  
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<400> 201  
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<210> 202  
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<212> PRT  
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<400> 202  
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Cys Phe Trp Val Leu Asp  
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<210> 203  
<211> 42  
<212> DNA  
<213> Homo Sapiens

<400> 203  
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<210> 204  
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<212> PRT  
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<400> 204  
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<210> 205  
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<212> DNA  
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<400> 205  
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<211> 12  
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<400> 206  
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<210> 207  
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<210> 208  
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<210> 209  
<211> 24  
<212> DNA  
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<400> 209  
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<400> 210  
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<400> 211  
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<400> 212  
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<211> 21  
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<400> 213  
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<400> 214  
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<210> 215  
<211> 42  
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<400> 215  
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<210> 216  
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<212> PRT  
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<400> 216  
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<212> DNA  
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<400> 218  
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<400> 224  
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<210> 226  
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<210> 227  
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tgttgctttg ttaccagacc taattga 87

<210> 228  
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<400> 228  
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20 25

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<211> 180  
<212> DNA  
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<210> 230  
 <211> 59  
 <212> PRT  
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<400> 230  
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 20 25 30  
 Cys Pro Phe Phe Leu Trp Ser Lys Thr Leu Leu Asn Phe Cys Lys Tyr  
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<210> 233  
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 <212> PRT  
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 1 5

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 <212> DNA  
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<210> 236  
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&lt;213&gt; Homo Sapiens

&lt;400&gt; 236

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His Pro Phe Ser Asn Met Tyr Leu Ser Ser His Tyr Phe Cys Phe Thr  
20 25 30  
Ala Val Leu Lys Asn Thr Tyr Tyr Ala Thr Asn Cys His Ile Ile Phe  
35 40 45  
Arg

&lt;210&gt; 237

&lt;211&gt; 54

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 237

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&lt;210&gt; 238

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 238

Met Pro Ser Arg His Leu Arg Ala Ile Leu Ile Pro Ser Ala Ile Cys  
1 5 10 15  
Ile

&lt;210&gt; 239

&lt;211&gt; 87

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 239

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accaattgtc atattatttt tagatga 87

&lt;210&gt; 240

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 240

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1 5 10 15  
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20 25

&lt;210&gt; 241

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 241

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&lt;210&gt; 242

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 242

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<210> 245  
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 <213> Homo Sapiens

<400> 246  
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 cctgaccacg ggcttcagcc gcatgagtga gcggcagggt gcgctgtggg acacaaagca 900  
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cacccatcca ctacactccc attcccagcc acatggcaga gaaaaaaatc ataataaat 1620
ggctttatct tctggtaaaa aaaaaaaaaa agggcggcc 1659

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&lt;210&gt; 248

&lt;211&gt; 1386

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 248

```

atgagccggc aggtggtccg ctccagcaag ttccgccacg tgtttggaca gccggccaag 60
gccgaccagt gctatgaaga tgtgcgcgtc tcacagacca cctgggacag tggcttctgt 120
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agtgtggact ggagccgaga tggaggcctc atttgtacct cctgccgtga caagcgcgtg 600
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caggccacgg tgcaggagct ccagaagcgc ttggacaggc tggaggagac agtccaggcc 1380
aagtag 1386

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&lt;210&gt; 249

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 249

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Met Ser Arg Gln Val Val Arg Ser Ser Lys Phe Arg His Val Phe Gly
 1          5          10         15
Gln Pro Ala Lys Ala Asp Gln Cys Tyr Glu Asp Val Arg Val Ser Gln
 20          25          30
Thr Thr Trp Asp Ser Gly Phe Cys Ala Val Asn Pro Lys Phe Val Ala
 35          40          45
Leu Ile Cys Glu Ala Ser Gly Gly Gly Ala Phe Leu Val Leu Pro Leu
 50          55          60
Gly Lys Thr Gly Arg Val Asp Lys Asn Ala Pro Thr Val Cys Gly His
 65          70          75          80
Thr Ala Pro Val Leu Asp Ile Ala Trp Cys Pro His Asn Asp Asn Val
 85          90          95
Ile Ala Ser Gly Ser Glu Asp Cys Thr Val Met Val Trp Glu Ile Pro
100         105         110
Asp Gly Gly Leu Met Leu Pro Leu Arg Glu Pro Val Val Thr Leu Glu

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115	120	125
Gly His Thr Lys Arg Val	Gly Ile Val Ala Trp	His Thr Thr Ala Gln
130	135	140
Asn Val Leu Leu Ser Ala	Gly Cys Asp Asn Val	Ile Met Val Trp Asp
145	150	155
Val Gly Thr Gly Ala Ala	Met Leu Thr Leu Gly	Pro Glu Val His Pro
165	170	175
Asp Thr Ile Tyr Ser Val	Asp Trp Ser Arg Asp	Gly Gly Leu Ile Cys
180	185	190
Thr Ser Cys Arg Asp Lys	Arg Val Arg Ile Ile	Glu Pro Arg Lys Gly
195	200	205
Thr Val Val Ala Glu Lys	Asp Arg Pro His Glu	Gly Thr Arg Pro Val
210	215	220
Arg Ala Val Phe Val Ser	Glu Gly Lys Ile Leu	Thr Thr Gly Phe Ser
225	230	235
Arg Met Ser Glu Arg Gln	Val Ala Leu Trp Asp	Thr Lys His Leu Glu
245	250	255
Glu Pro Leu Ser Leu Gln	Glu Leu Asp Thr Ser	Ser Gly Val Leu Leu
260	265	270
Pro Phe Phe Asp Pro Asp	Thr Asn Ile Val Tyr	Leu Cys Gly Lys Gly
275	280	285
Asp Ser Ser Ile Arg Tyr	Phe Glu Ile Thr Ser	Glu Ala Pro Phe Leu
290	295	300
His Tyr Leu Ser Met Phe	Ser Ser Lys Glu Ser	Gln Arg Gly Met Gly
305	310	315
Tyr Met Pro Lys Arg Gly	Leu Glu Val Asn Lys	Cys Glu Ile Ala Arg
325	330	335
Phe Tyr Lys Leu His Glu	Arg Arg Cys Glu Pro	Ile Ala Met Thr Val
340	345	350
Pro Arg Lys Ser Asp Leu	Phe Gln Glu Asp Leu	Tyr Pro Pro Thr Ala
355	360	365
Gly Pro Asp Pro Ala Leu	Thr Ala Glu Glu Trp	Leu Gly Gly Arg Asp
370	375	380
Ala Gly Pro Leu Leu Ile	Ser Leu Lys Asp Gly	Tyr Val Pro Pro Lys
385	390	395
Ser Arg Glu Leu Arg Val	Asn Arg Gly Leu Asp	Thr Gly Arg Arg Arg
405	410	415
Ala Ala Pro Glu Ala Ser	Gly Thr Pro Ser Ser	Asp Ala Val Ser Arg
420	425	430
Leu Glu Glu Glu Met Arg	Lys Leu Gln Ala Thr	Val Gln Glu Leu Gln
435	440	445
Lys Arg Leu Asp Arg Leu	Glu Glu Thr Val Gln	Ala Lys
450	455	460

&lt;210&gt; 250

&lt;211&gt; 75

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 250

atgaagatgt ggcgcgtctca cagaccacct gggacagtgg cttctgtgct gtcaacccta  
agtttgtggc cctga

60

75

&lt;210&gt; 251

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 251

Met Lys Met Cys Ala Ser His Arg Pro Pro Gly Thr Val Ala Ser Val  
1 5 10 15  
Leu Ser Thr Leu Ser Leu Trp Pro  
20

&lt;210&gt; 252

<211> 69  
 <212> DNA  
 <213> Homo Sapiens

<400> 252  
 atgtgcgcgt ctcacagacc acctgggaca gtggcttctg tgctgtcaac cctaagtttg 60  
 tggccctga 69

<210> 253  
 <211> 22  
 <212> PRT  
 <213> Homo Sapiens

<400> 253  
 Met Cys Ala Ser His Arg Pro Pro Gly Thr Val Ala Ser Val Leu Ser  
 1 5 10 15  
 Thr Leu Ser Leu Trp Pro  
 20

<210> 254  
 <211> 39  
 <212> DNA  
 <213> Homo Sapiens

<400> 254  
 atgcgcccac ggtctgtggc cacacagccc ctgtgctag 39

<210> 255  
 <211> 12  
 <212> PRT  
 <213> Homo Sapiens

<400> 255  
 Met Arg Pro Arg Ser Val Ala Thr Gln Pro Leu Cys  
 1 5 10

<210> 256  
 <211> 72  
 <212> DNA  
 <213> Homo Sapiens

<400> 256  
 atgacaacgt cattgccagt ggctccgagg actgcacagt catggtgtgg gagatcccag 60  
 atggggcct ga 72

<210> 257  
 <211> 23  
 <212> PRT  
 <213> Homo Sapiens

<400> 257  
 Met Thr Thr Ser Leu Pro Val Ala Pro Arg Thr Ala Gln Ser Trp Cys  
 1 5 10 15  
 Gly Arg Ser Gln Met Gly Ala  
 20

<210> 258  
 <211> 1068  
 <212> DNA  
 <213> Homo Sapiens

<400> 258  
 atggtgtggg agatcccaga tgggggcctg atgctgcccc tgcgggagcc cgtcgtcacc 60  
 ctggagggcc acaccaagcg tgtgggcatt gtggcctggc acaccacagc ccagaacgtg 120  
 ctgctcagtg caggttgtga caacgtgatc atggtgtggg acgtgggcac tggggcggcc 180

atgctgacac	tgggcccaga	ggtgcaccca	gacacgatct	acagtgtgga	ctggagccga	240
gatggaggcc	tcatttgtac	ctcctgccgt	gacaagcgcg	tgcgcatcat	cgagccccgc	300
aaaggcactg	tcgtagctga	gaaggaccgt	ccccacgagg	ggacccggcc	cgtgcgtgca	360
gtgttcgtgt	cggaggggaa	gatcctgacc	acgggcttca	gccgcatgag	tgagcggcag	420
gtggcgctgt	gggacacaaa	gcacctggag	gagccgctgt	ccctgcagga	gctggacacc	480
agcagcggtg	tcctgctgcc	cttctttgac	cctgacacca	acatcgtcta	cctctgtggc	540
aagggtgaca	gctcaatccg	gtactttgag	atcacttccg	aggccctttt	cctgcactat	600
ctctccatgt	tcagttccaa	ggagtccag	cggggcatgg	gctacatgcc	caaacgtggc	660
ctggaggtga	acaagtgtga	gatcgccagg	ttctacaagc	tgacagagcg	gaggtgtgag	720
cccattgcca	tgacagtgcc	tcgaaagtcg	gacctgttcc	aggaggacct	gtacccaccc	780
accgcagggc	ccgacctgc	cctcacggct	gaggagtggc	tgggggggtcg	ggatgctggg	840
cccttcctca	tctccctcaa	ggatggctac	gtacccccaa	agagccggga	gctgagggtc	900
aaaccggggc	tggacaccgg	gcgcaggagg	gcagcacccag	aggccagtgg	cactcccgagc	960
tcggatgccg	tgtctcggct	ggaggaggag	atgcggaagc	tccaggccac	ggtgcaggag	1020
ctccagaagc	gcttgacag	gctggaggag	acagtccagg	ccaagtag		1068

&lt;210&gt; 259

&lt;211&gt; 355

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 259

Met	Val	Trp	Glu	Ile	Pro	Asp	Gly	Gly	Leu	Met	Leu	Pro	Leu	Arg	Glu
1				5					10					15	
Pro	Val	Val	Thr	Leu	Glu	Gly	His	Thr	Lys	Arg	Val	Gly	Ile	Val	Ala
			20					25					30		
Trp	His	Thr	Thr	Ala	Gln	Asn	Val	Leu	Leu	Ser	Ala	Gly	Cys	Asp	Asn
		35				40					45				
Val	Ile	Met	Val	Trp	Asp	Val	Gly	Thr	Gly	Ala	Ala	Met	Leu	Thr	Leu
	50				55						60				
Gly	Pro	Glu	Val	His	Pro	Asp	Thr	Ile	Tyr	Ser	Val	Asp	Trp	Ser	Arg
65				70					75					80	
Asp	Gly	Gly	Leu	Ile	Cys	Thr	Ser	Cys	Arg	Asp	Lys	Arg	Val	Arg	Ile
			85					90					95		
Ile	Glu	Pro	Arg	Lys	Gly	Thr	Val	Val	Ala	Glu	Lys	Asp	Arg	Pro	His
		100					105						110		
Glu	Gly	Thr	Arg	Pro	Val	Arg	Ala	Val	Phe	Val	Ser	Glu	Gly	Lys	Ile
		115				120						125			
Leu	Thr	Thr	Gly	Phe	Ser	Arg	Met	Ser	Glu	Arg	Gln	Val	Ala	Leu	Trp
	130					135					140				
Asp	Thr	Lys	His	Leu	Glu	Pro	Leu	Ser	Leu	Gln	Glu	Leu	Asp	Thr	
145				150				155					160		
Ser	Ser	Gly	Val	Leu	Leu	Pro	Phe	Phe	Asp	Pro	Asp	Thr	Asn	Ile	Val
			165					170					175		
Tyr	Leu	Cys	Gly	Lys	Gly	Asp	Ser	Ser	Ile	Arg	Tyr	Phe	Glu	Ile	Thr
		180					185					190			
Ser	Glu	Ala	Pro	Phe	Leu	His	Tyr	Leu	Ser	Met	Phe	Ser	Ser	Lys	Glu
	195					200					205				
Ser	Gln	Arg	Gly	Met	Gly	Tyr	Met	Pro	Lys	Arg	Gly	Leu	Glu	Val	Asn
	210					215					220				
Lys	Cys	Glu	Ile	Ala	Arg	Phe	Tyr	Lys	Leu	His	Glu	Arg	Arg	Cys	Glu
225				230					235					240	
Pro	Ile	Ala	Met	Thr	Val	Pro	Arg	Lys	Ser	Asp	Leu	Phe	Gln	Glu	Asp
			245					250					255		
Leu	Tyr	Pro	Pro	Thr	Ala	Gly	Pro	Asp	Pro	Ala	Leu	Thr	Ala	Glu	Glu
		260				265						270			
Trp	Leu	Gly	Gly	Arg	Asp	Ala	Gly	Pro	Leu	Leu	Ile	Ser	Leu	Lys	Asp
	275					280					285				
Gly	Tyr	Val	Pro	Pro	Lys	Ser	Arg	Glu	Leu	Arg	Val	Asn	Arg	Gly	Leu
	290				295						300				
Asp	Thr	Gly	Arg	Arg	Arg	Ala	Ala	Pro	Glu	Ala	Ser	Gly	Thr	Pro	Ser
305				310					315					320	
Ser	Asp	Ala	Val	Ser	Arg	Leu	Glu	Glu	Glu	Met	Arg	Lys	Leu	Gln	Ala
			325					330					335		
Thr	Val	Gln	Glu	Leu	Gln	Lys	Arg	Leu	Asp	Arg	Leu	Glu	Glu	Thr	Val

Gln Ala Lys  
355

345

350

<210> 260  
<211> 12  
<212> DNA  
<213> Homo Sapiens

<400> 260  
atgggggcct ga

12

<210> 261  
<211> 3  
<212> PRT  
<213> Homo Sapiens

<400> 261  
Met Gly Ala  
1

<210> 262  
<211> 1038  
<212> DNA  
<213> Homo Sapiens

<400> 262  
atgctgcccc tgcgggagcc cgtcgtcacc ctggaggggcc acaccaagcg tgtgggcatt 60  
gtggcctggc acaccacagc ccagaacgtg ctgctcagtg caggttgtga caacgtgac 120  
atggtgtggg acgtgggcac tggggcgggc atgctgacac tgggccaga ggtgcaccca 180  
gacacgatct acagtgtgga ctggagccga gatggaggcc tcatttgtac ctctgcccgt 240  
gacaagcgcg tgcgcacat cgagcccgcc gtgttcgtgt gtgttcgtgt cggaggggaa gatcctgacc 300  
ccccacgagg ggacccggcc cgtgcgtgca gtgttcgtgt gtgttcgtgt gggacacaaa gcacctggag 360  
acgggcttca gccgcatgag tgagcggcag gtggcgctgt gggacacaaa gcacctggag 420  
gagccgctgt ccctgcagga gctggacacc agcagcggtg tcctgctgcc cttctttgac 480  
cctgacacca acatcgtcta cctctgtggc aagggtgaca gctcaatccg gtactttgag 540  
atcacttccg agggcccttt cctgcactat ctctccatgt tcagttccaa ggagtcccag 600  
cggggcatgg gctacatgcc caaacgtggc ctggagggtga acaagtgtga gatcgccagg 660  
ttctacaagc tgcacgagcg gaggtgtgag cccattgcca tgacagtgcc tcgaaagtcg 720  
gacctgttcc aggaggacct gtacccaccc accgcagggc ccgacctgc cctcacggct 780  
gaggagtggc tgggggggtcg ggatgctggg cccctcctca tctccctcaa ggatggctac 840  
gtaccccaaa agagccggga gctgagggtc aaccggggcc tggacaccgg gcgcaggagg 900  
gcagcaccag aggccagtgg cactcccagc tcggatgccg tgtctcggtt ggaggaggag 960  
atgcggaagc tccaggccac ggtgcaggag ctccagaagc gcttgagacg gctggaggag 1020  
acagtccagg ccaagtag 1038

<210> 263  
<211> 345  
<212> PRT  
<213> Homo Sapiens

<400> 263  
Met Leu Pro Leu Arg Glu Pro Val Val Thr Leu Glu Gly His Thr Lys  
1 5 10 15  
Arg Val Gly Ile Val Ala Trp His Thr Thr Ala Gln Asn Val Leu Leu  
20 25 30  
Ser Ala Gly Cys Asp Asn Val Ile Met Val Trp Asp Val Gly Thr Gly  
35 40 45  
Ala Ala Met Leu Thr Leu Gly Pro Glu Val His Pro Asp Thr Ile Tyr  
50 55 60  
Ser Val Asp Trp Ser Arg Asp Gly Gly Leu Ile Cys Thr Ser Cys Arg  
65 70 75 80  
Asp Lys Arg Val Arg Ile Ile Glu Pro Arg Lys Gly Thr Val Val Ala  
85 90 95  
Glu Lys Asp Arg Pro His Glu Gly Thr Arg Pro Val Arg Ala Val Phe

45/60

```
<210> 264
<211> 918
<212> DNA
<213> Homo Sapiens
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<400>	264						
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gacacgatct	acagtgtgga	ctggagccga	gatggaggcg	tcatattgtac	ctcctgccgt		120
gacaagcgcg	tgcgcatact	cgagccccgc	aaaggcactc	tcgtagtctga	gaaggaccgt		180
ccccacgag	ggacccggcc	cgctgcgtgca	gtgtctcgtgt	cggaggggaa	gacctgacc		240
acgggcttca	gccgcatagag	tgagcggcag	gtggcgctgt	gggacacaaa	gcacctggag		300
gagccgctgt	ccctgcagga	gctggacacc	agcagcgtgt	tctgtctgcc	cttctttgac		360
cctgacacca	acatcgtcta	cctctgtggc	aagggtgaca	gctcaatccg	gtactttgag		420
atcactttccg	aggccccctt	cctgcactat	ctctccatgt	tcagttccaa	ggagtcccag		480
cggggctatg	gctacatgcc	caaacgtggc	ctggagggtga	acaagtgtga	gatcgccagg		540
ttctacaagc	tgcacgagcg	gaggtgtgag	cccattgcc	tgacagtgcc	tcgaaagtgc		600
gacctgttcc	aggaggacct	gtacccaccc	accgcagggc	ccgacctgc	cctcacggct		660
gaggagtggc	tggggggctg	ggatgctggg	cccctcctca	tctccctcaa	ggatggctac		720
gtacccccaa	agagccggga	gctgagggtc	aaccggggcc	tggacaccgg	gcgcaggagg		780
gcagcaccag	aggccagtgg	cactcccagc	tcgatgccc	tgtctcgggt	ggaggaggag		840
atgcggaagc	tccaggccac	ggtgcaggag	ctccagaagc	gcttggacag	gctggaggag		900
acagtccagg	ccaagttag						918

```
<210> 265
<211> 305
<212> PRT
<213> Homo Sapiens
```

```

<400> 265
Met Val Trp Asp Val Gly Thr Gly Ala Ala Met Leu Thr Leu Gly Pro
 1          5          10          15
Glu Val His Pro Asp Thr Ile Tyr Ser Val Asp Trp Ser Arg Asp Gly
      20          25          30

```



46/60

Gly Leu Ile Cys Thr Ser Cys Arg Asp Lys Arg Val Arg Ile Ile Glu  
 35 40 45  
 Pro Arg Lys Gly Thr Val Val Ala Glu Lys Asp Arg Pro His Glu Gly  
 50 55 60  
 Thr Arg Pro Val Arg Ala Val Phe Val Ser Glu Lys Ile Leu Thr  
 65 70 75 80  
 Thr Gly Phe Ser Arg Met Ser Glu Arg Gln Val Ala Leu Trp Asp Thr  
 85 90 95  
 Lys His Leu Glu Glu Pro Leu Ser Leu Gln Glu Leu Asp Thr Ser Ser  
 100 105 110  
 Gly Val Leu Leu Pro Phe Phe Asp Pro Asp Thr Asn Ile Val Tyr Leu  
 115 120 125  
 Cys Gly Lys Gly Asp Ser Ser Ile Arg Tyr Phe Glu Ile Thr Ser Glu  
 130 135 140  
 Ala Pro Phe Leu His Tyr Leu Ser Met Phe Ser Ser Lys Glu Ser Gln  
 145 150 155 160  
 Arg Gly Met Gly Tyr Met Pro Lys Arg Gly Leu Glu Val Asn Lys Cys  
 165 170 175  
 Glu Ile Ala Arg Phe Tyr Lys Leu His Glu Arg Arg Cys Glu Pro Ile  
 180 185 190  
 Ala Met Thr Val Pro Arg Lys Ser Asp Leu Phe Gln Glu Asp Leu Tyr  
 195 200 205  
 Pro Pro Thr Ala Gly Pro Asp Pro Ala Leu Thr Ala Glu Glu Trp Leu  
 210 215 220  
 Gly Gly Arg Asp Ala Gly Pro Leu Leu Ile Ser Leu Lys Asp Gly Tyr  
 225 230 235 240  
 Val Pro Pro Lys Ser Arg Glu Leu Arg Val Asn Arg Gly Leu Asp Thr  
 245 250 255  
 Gly Arg Arg Arg Ala Ala Pro Glu Ala Ser Gly Thr Pro Ser Ser Asp  
 260 265 270  
 Ala Val Ser Arg Leu Glu Glu Glu Met Arg Lys Leu Gln Ala Thr Val  
 275 280 285  
 Gln Glu Leu Gln Lys Arg Leu Asp Arg Leu Glu Glu Thr Val Gln Ala  
 290 295 300  
 Lys  
 305

&lt;210&gt; 266

&lt;211&gt; 888

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 266

atgctgacac	tgggcccaga	ggtgcaccca	gacacgatct	acagtgtgga	ctggagccga	60
gatggaggcc	tcatttgtac	ctcctgccgt	gacaagcgcg	tgcgcatcat	cgagccccgc	120
aaaggcactg	tcgtagctga	gaaggaccgt	ccccacgagg	ggacccggcc	cgtgcgtgca	180
gtgttcgtgt	cggaggggaa	gaccttgacc	acgggcttca	gccgcatgag	tgagcggcag	240
gtggcgctgt	gggacacaaa	gcacctggag	gagccgctgt	ccctgcagga	gctggacacc	300
agcagcgggtg	tcctgctgcc	cttctttgac	cctgacacca	acatcgtcta	cctctgtggc	360
aagggtgaca	gctcaatccg	gtactttgag	atcacttccg	aggccccttt	cctgcactat	420
ctctccatgt	tcagttccaa	ggagtcccag	cggggcatgg	gctacatgcc	caaacgtggc	480
ctggaggtga	acaagtgtga	gatcgccagg	ttctacaagc	tgcacgagcg	gaggtgtgag	540
cccattgcc	tgacagtgcc	tcgaaagtgc	gacctgttcc	aggaggacct	gtaccacccc	600
accgcagggc	ccgaccctgc	cctcacggct	gaggagtggc	tgggggggtcg	ggatgctggg	660
cccctcctca	tctccctcaa	ggatggctac	gtacccccaa	agagccggga	gctgaggggtc	720
aaccggggcc	tggacaccgg	gcgcaggagg	gcagcaccag	aggccagtgg	cactcccagc	780
tcggatgccg	tgtctcggct	ggaggaggag	atgcggaagc	tccaggccac	ggtgcaggag	840
ctccagaagc	gcttggacag	gctggaggag	acagtccagg	ccaagtag		888

&lt;210&gt; 267

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 267

47/60

Met Leu Thr Leu Gly Pro Glu Val His Pro Asp Thr Ile Tyr Ser Val  
 1 5 10 15  
 Asp Trp Ser Arg Asp Gly Gly Leu Ile Cys Thr Ser Cys Arg Asp Lys  
 20 25 30  
 Arg Val Arg Ile Ile Glu Pro Arg Lys Gly Thr Val Val Ala Glu Lys  
 35 40 45  
 Asp Arg Pro His Glu Gly Thr Arg Pro Val Arg Ala Val Phe Val Ser  
 50 55 60  
 Glu Gly Lys Ile Leu Thr Thr Gly Phe Ser Arg Met Ser Glu Arg Gln  
 65 70 75 80  
 Val Ala Leu Trp Asp Thr Lys His Leu Glu Glu Pro Leu Ser Leu Gln  
 85 90 95  
 Glu Leu Asp Thr Ser Ser Gly Val Leu Leu Pro Phe Phe Asp Pro Asp  
 100 105 110  
 Thr Asn Ile Val Tyr Leu Cys Gly Lys Gly Asp Ser Ser Ile Arg Tyr  
 115 120 125  
 Phe Glu Ile Thr Ser Glu Ala Pro Phe Leu His Tyr Leu Ser Met Phe  
 130 135 140  
 Ser Ser Lys Glu Ser Gln Arg Gly Met Gly Tyr Met Pro Lys Arg Gly  
 145 150 155 160  
 Leu Glu Val Asn Lys Cys Glu Ile Ala Arg Phe Tyr Lys Leu His Glu  
 165 170 175  
 Arg Arg Cys Glu Pro Ile Ala Met Thr Val Pro Arg Lys Ser Asp Leu  
 180 185 190  
 Phe Gln Glu Asp Leu Tyr Pro Pro Thr Ala Gly Pro Asp Pro Ala Leu  
 195 200 205  
 Thr Ala Glu Glu Trp Leu Gly Gly Arg Asp Ala Gly Pro Leu Leu Ile  
 210 215 220  
 Ser Leu Lys Asp Gly Tyr Val Pro Pro Lys Ser Arg Glu Leu Arg Val  
 225 230 235 240  
 Asn Arg Gly Leu Asp Thr Gly Arg Arg Arg Ala Ala Pro Glu Ala Ser  
 245 250 255  
 Gly Thr Pro Ser Ser Asp Ala Val Ser Arg Leu Glu Glu Glu Met Arg  
 260 265 270  
 Lys Leu Gln Ala Thr Val Gln Glu Leu Gln Lys Arg Leu Asp Arg Leu  
 275 280 285  
 Glu Glu Thr Val Gln Ala Lys  
 290 295

&lt;210&gt; 268

&lt;211&gt; 75

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 268

atggaggcct catttgtagc tccctgccgtg acaagcgcgt gcgcatcatc gagccccgca  
 aaggcactgt cgtag

60

75

&lt;210&gt; 269

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 269

Met Glu Ala Ser Phe Val Pro Pro Ala Val Thr Ser Ala Cys Ala Ser  
 1 5 10 15  
 Ser Ser Pro Ala Lys Ala Leu Ser  
 20

&lt;210&gt; 270

&lt;211&gt; 663

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 270

48/60

```

atgagtgagc ggcaggtggc gctgtgggac acaaagcacc tggaggagcc gctgtccctg      60
caggagctgg acaccagcag cgggtgtcctg ctgcccttct ttgaccctga caccaacatc      120
gtctacctct gtggcaagggt tgacagctca atccggtact ttgagatcac ttccgaggcc      180
cctttctctg actatctctc catgttcagt tccaaggagt cccagcgggg catgggctac      240
atgccccaaac gtggcctgga ggtgaacaag tgtgagatcg ccagggtcta caagctgcac      300
gagcggaggt gtgagcccat tgccatgaca gtgcctcgaa agtcggacct gttccaggag      360
gacctgtacc caccaccgc agggcccgac cctgccctca cggctgagga gtggctgggg      420
ggtcgggatg ctgggccctt cctcatctcc ctcaaggatg gctacgtacc cccaaagagc      480
cgggagctga ggggtcaaccg gggcctggac accgggcgca ggagggcagc accagaggcc      540
agtggcactc ccagctcgga tgccgtgtct cggctggagg aggagatgcg gaagctccag      600
gccacggtgc aggagctcca gaagcgcttg gacaggctgg aggagacagt ccaggccaag      660
tag

```

&lt;210&gt; 271

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 271

```

Met Ser Glu Arg Gln Val Ala Leu Trp Asp Thr Lys His Leu Glu Glu
 1          5          10          15
Pro Leu Ser Leu Gln Glu Leu Asp Thr Ser Ser Gly Val Leu Leu Pro.
 20          25          30
Phe Phe Asp Pro Asp Thr Asn Ile Val Tyr Leu Cys Gly Lys Gly Asp
 35          40          45
Ser Ser Ile Arg Tyr Phe Glu Ile Thr Ser Glu Ala Pro Phe Leu His
 50          55          60
Tyr Leu Ser Met Phe Ser Ser Lys Glu Ser Gln Arg Gly Met Gly Tyr
 65          70          75          80
Met Pro Lys Arg Gly Leu Glu Val Asn Lys Cys Glu Ile Ala Arg Phe
 85          90          95
Tyr Lys Leu His Glu Arg Arg Cys Glu Pro Ile Ala Met Thr Val Pro
100          105          110
Arg Lys Ser Asp Leu Phe Gln Glu Asp Leu Tyr Pro Pro Thr Ala Gly
115          120          125
Pro Asp Pro Ala Leu Thr Ala Glu Glu Trp Leu Gly Gly Arg Asp Ala
130          135          140
Gly Pro Leu Leu Ile Ser Leu Lys Asp Gly Tyr Val Pro Pro Lys Ser
145          150          155          160
Arg Glu Leu Arg Val Asn Arg Gly Leu Asp Thr Gly Arg Arg Arg Ala
165          170          175
Ala Pro Glu Ala Ser Gly Thr Pro Ser Ser Asp Ala Val Ser Arg Leu
180          185          190
Glu Glu Glu Met Arg Lys Leu Gln Ala Thr Val Gln Glu Leu Gln Lys
195          200          205
Arg Leu Asp Arg Leu Glu Glu Thr Val Gln Ala Lys
210          215          220

```

&lt;210&gt; 272

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 272

```

atgttcagtt ccaaggagtc ccagcggggc atgggctaca tgcccaaagc tggcctggag      60
gtgaacaagt gtgagatcgc caggttctac aagctgcacg agcggagggtg tgagcccatt      120
gccatgacag tgccctgaaa gtcggacctg ttccaggagg acctgtaccc acccaccgca      180
gggcccagacc ctgccctcac ggctgaggag tggctggggg gtcgggatgc tggggccctc      240
ctcatctccc tcaaggatgg ctacgtaccc ccaaagagcc gggagctgag ggtcaaccgg      300
ggcctggaca ccgggcgcag gagggcagca ccagaggcca gtggcactcc cagctcggat      360
gccgtgtctc ggctggagga ggagatgcgg aagctccagg ccacggtgca ggagctccag      420
aagcgcttgg acaggctgga ggagacagtc caggccaagt ag      462

```

&lt;210&gt; 273

&lt;211&gt; 153

49/60

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 273

```

Met Phe Ser Ser Lys Glu Ser Gln Arg Gly Met Gly Tyr Met Pro Lys
 1          5          10          15
Arg Gly Leu Glu Val Asn Lys Cys Glu Ile Ala Arg Phe Tyr Lys Leu
          20          25          30
His Glu Arg Arg Cys Glu Pro Ile Ala Met Thr Val Pro Arg Lys Ser
          35          40          45
Asp Leu Phe Gln Glu Asp Leu Tyr Pro Pro Thr Ala Gly Pro Asp Pro
          50          55          60
Ala Leu Thr Ala Glu Glu Trp Leu Gly Gly Arg Asp Ala Gly Pro Leu
          65          70          75          80
Leu Ile Ser Leu Lys Asp Gly Tyr Val Pro Pro Lys Ser Arg Glu Leu
          85          90          95
Arg Val Asn Arg Gly Leu Asp Thr Gly Arg Arg Arg Ala Ala Pro Glu
          100          105          110
Ala Ser Gly Thr Pro Ser Ser Asp Ala Val Ser Arg Leu Glu Glu Glu
          115          120          125
Met Arg Lys Leu Gln Ala Thr Val Gln Glu Leu Gln Lys Arg Leu Asp
          130          135          140
Arg Leu Glu Glu Thr Val Gln Ala Lys
          145          150

```

&lt;210&gt; 274

&lt;211&gt; 432

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 274

```

atgggctaca tgcccaaagc tggcctggag gtgaacaagt gtgagatcgc caggttctac      60
aagctgcacg agcggagggt tgagcccatt gccatgacag tgcctcgaaa gtcggacctg      120
ttccaggagg acctgtaccc acccaccgca gggcccgacc ctgccctcac ggctgaggag      180
tggtcggggg gtcgggatgc tgggcccctc ctcactctcc tcaaggatgg ctacgtaccc      240
ccaaagagcc gggagctgag ggtcaaccgg ggctggaca ccgggcgcag gagggcagca      300
ccagaggcca gtggcactcc cagctcggat gccgtgtctc ggctggagga ggagatgcgg      360
aagctccagg ccacggtgca ggagctccag aagcgcttgg acaggctgga ggagacagtc      420
caggccaagt ag                                     432

```

&lt;210&gt; 275

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 275

```

Met Gly Tyr Met Pro Lys Arg Gly Leu Glu Val Asn Lys Cys Glu Ile
 1          5          10          15
Ala Arg Phe Tyr Lys Leu His Glu Arg Arg Cys Glu Pro Ile Ala Met
          20          25          30
Thr Val Pro Arg Lys Ser Asp Leu Phe Gln Glu Asp Leu Tyr Pro Pro
          35          40          45
Thr Ala Gly Pro Asp Pro Ala Leu Thr Ala Glu Glu Trp Leu Gly Gly
          50          55          60
Arg Asp Ala Gly Pro Leu Leu Ile Ser Leu Lys Asp Gly Tyr Val Pro
          65          70          75          80
Pro Lys Ser Arg Glu Leu Arg Val Asn Arg Gly Leu Asp Thr Gly Arg
          85          90          95
Arg Arg Ala Ala Pro Glu Ala Ser Gly Thr Pro Ser Ser Asp Ala Val
          100          105          110
Ser Arg Leu Glu Glu Glu Met Arg Lys Leu Gln Ala Thr Val Gln Glu
          115          120          125
Leu Gln Lys Arg Leu Asp Arg Leu Glu Glu Thr Val Gln Ala Lys
          130          135          140

```

<210> 276  
 <211> 423  
 <212> DNA  
 <213> Homo Sapiens

<400> 276  
 atgccccaaac gtggcctgga ggtgaacaag tgtgagatcg ccagggttcta caagctgcac 60  
 gagcggaggt gtgagcccat tgccatgaca gtgcctcgaa agtcggacct gttccaggag 120  
 gacctgtacc caccaccgc agggcccgc cctgccctca cggctgagga gtggctgggg 180  
 ggtcgggatg ctggggccct cctcatctcc ctcaaggatg gctacgtacc cccaaagagc 240  
 cgggagctga gggcacaacc gggcctggac accgggcgca ggagggcagc accagaggcc 300  
 agtggcactc ccagctcgga tgccgtgtct cggctggagg aggagatcg gaagctccag 360  
 gccacggtgc aggagctcca gaagcgcttg gacaggctgg aggagacagt ccaggccaag 420  
 tag 423

<210> 277  
 <211> 140  
 <212> PRT  
 <213> Homo Sapiens

<400> 277  
 Met Pro Lys Arg Gly Leu Glu Val Asn Lys Cys Glu Ile Ala Arg Phe  
 1 5 10 15  
 Tyr Lys Leu His Glu Arg Arg Cys Glu Pro Ile Ala Met Thr Val Pro  
 20 25 30  
 Arg Lys Ser Asp Leu Phe Gln Glu Asp Leu Tyr Pro Pro Thr Ala Gly  
 35 40 45  
 Pro Asp Pro Ala Leu Thr Ala Glu Glu Trp Leu Gly Gly Arg Asp Ala  
 50 55 60  
 Gly Pro Leu Leu Ile Ser Leu Lys Asp Gly Tyr Val Pro Pro Lys Ser  
 65 70 75 80  
 Arg Glu Leu Arg Val Asn Arg Gly Leu Asp Thr Gly Arg Arg Arg Ala  
 85 90 95  
 Ala Pro Glu Ala Ser Gly Thr Pro Ser Ser Asp Ala Val Ser Arg Leu  
 100 105 110  
 Glu Glu Glu Met Arg Lys Leu Gln Ala Thr Val Gln Glu Leu Gln Lys  
 115 120 125  
 Arg Leu Asp Arg Leu Glu Glu Thr Val Gln Ala Lys  
 130 135 140

<210> 278  
 <211> 339  
 <212> DNA  
 <213> Homo Sapiens

<400> 278  
 atgacagtgc ctcgaaagtc ggacctgttc caggaggacc tgtaccacc caccgcaggg 60  
 cccgaccctg ccctcacggc tgaggagtgg ctgggggggtc gggatgctgg gccctcctc 120  
 atctccctca aggatggcta cgtaccccca aagagccggg agctgagggt caaccggggc 180  
 ctggacaccg ggcgcaggag ggcagcacca gaggccagtg gcactcccag ctcggtatgcc 240  
 gtgtctcggc tggaggagga gatgcggaag ctccaggcca cgggtgcagga gctccagaag 300  
 cgcttgagca ggctggagga gacagtccag gccaaagtag 339

<210> 279  
 <211> 112  
 <212> PRT  
 <213> Homo Sapiens

<400> 279  
 Met Thr Val Pro Arg Lys Ser Asp Leu Phe Gln Glu Asp Leu Tyr Pro  
 1 5 10 15  
 Pro Thr Ala Gly Pro Asp Pro Ala Leu Thr Ala Glu Glu Trp Leu Gly  
 20 25 30  
 Gly Arg Asp Ala Gly Pro Leu Leu Ile Ser Leu Lys Asp Gly Tyr Val  
 35 40 45

51/60

Pro Pro Lys Ser Arg Glu Leu Arg Val Asn Arg Gly Leu Asp Thr Gly  
           50                          55                          60  
 Arg Arg Arg Ala Ala Pro Glu Ala Ser Gly Thr Pro Ser Ser Asp Ala  
 65                          70                          75                          80  
 Val Ser Arg Leu Glu Glu Met Arg Lys Leu Gln Ala Thr Val Gln  
                           85                          90                          95  
 Glu Leu Gln Lys Arg Leu Asp Arg Leu Glu Glu Thr Val Gln Ala Lys  
                           100                          105                          110

<210> 280  
 <211> 63  
 <212> DNA  
 <213> Homo Sapiens

<400> 280  
 atgctgggccc cctcctcatc tccctcaagg atggctacgt acccccaaag agccgggagc 60  
 tga 63

<210> 281  
 <211> 20  
 <212> PRT  
 <213> Homo Sapiens

<400> 281  
 Met Leu Gly Pro Ser Ser Ser Pro Ser Arg Met Ala Thr Tyr Pro Gln  
   1                          5                          10                          15  
 Arg Ala Gly Ser  
                           20

<210> 282  
 <211> 33  
 <212> DNA  
 <213> Homo Sapiens

<400> 282  
 atggctacgt acccccaaag agccgggagc tga 33

<210> 283  
 <211> 10  
 <212> PRT  
 <213> Homo Sapiens

<400> 283  
 Met Ala Thr Tyr Pro Gln Arg Ala Gly Ser  
   1                          5                          10

<210> 284  
 <211> 238  
 <212> DNA  
 <213> Homo Sapiens

<400> 284  
 atgccgtgtc tcggctggag gaggagatgc ggaagctcca ggccacggtg caggagctcc 60  
 agaagcgctt ggacaggctg gaggagacag tccaggccaa gtagagcccc gcagggcctc 120  
 cagcagggtc agccattcac acccatccac tcacctcca ttcccagcca catggcagag 180  
 aaaaaaatca taataaaatg gctttatatt ctggtataaaa aaaaaaaaaa gggcggcc 238

<210> 285  
 <211> 79  
 <212> PRT  
 <213> Homo Sapiens

<400> 285  
 Met Pro Cys Leu Gly Trp Arg Arg Arg Cys Gly Ser Ser Arg Pro Arg  
   1                          5                          10                          15

Cys	Arg	Ser	Ser	Arg	Ser	Ala	Trp	Thr	Gly	Trp	Arg	Arg	Gln	Ser	Arg
			20					25					30		
Pro	Ser	Arg	Ala	Pro	Gln	Gly	Leu	Gln	Gln	Gly	Gln	Pro	Phe	Thr	Pro
		35					40					45			
Ile	His	Ser	Pro	Pro	Ile	Pro	Ser	His	Met	Ala	Glu	Lys	Lys	Ile	Ile
	50					55					60				
Ile	Lys	Trp	Leu	Tyr	Phe	Leu	Val	Lys	Lys	Lys	Lys	Lys	Gly	Gly	
65					70					75					

```
<210> 286
<211> 78
<212> DNA
<213> Homo Sapiens
```

```
<400> 386
atgcggaagc tccaggccac ggtgcaggag ctccagaagc gcttggacag gctggaggag    60
acaqtccagg ccaagtag                                     78
```

```
<210> 287
<211> 25
<212> PRT
<213> Homo Sapiens
```

```

<400> 287
Met Arg Lys Leu Gln Ala Thr Val Gln Glu Leu Gln Lys Arg Leu Asp
 1          5          10          15
Arg Leu Glu Glu Thr Val Gln Ala Lys
      20      25

```

```
<210> 288
<211> 67
<212> DNA
<213> Homo Sapiens
```

```
<400> 288
atggcgagaga aaaaaatcat aataaaatgg ctttattttc tggtaaaaaa aaaaaaaaag    60
ggcggcc                                           67
```

```
<210> 289
<211> 22
<212> PRT
<213> Homo Sapiens
```

```
<400> 289
Met Ala Glu Lys Lys Ile Ile Ile Lys Trp Leu Tyr Phe Leu Val Lys
  1             5             10             15
Lys Lys Lys Lys Gly Gly
      20
```

```
<210> 290
<211> 41
<212> DNA
<213> Homo Sapiens
```

<400> 290  
atggcctttat tttctggtaa aaaaaaaaaa aaagggcggc c 41

```
<210> 291
<211> 13
<212> PRT
<213> Homo Sapiens
```

<400> 291  
Met Ala Leu Phe Ser Gly Lys Lys Lys Lys Lys Gly Arg  
1 5 10

<210> 292  
 <211> 722  
 <212> DNA  
 <213> Homo Sapiens

```

<400> 292
tcgacccacg cgtccgctct gccgcagcct gtgccgcgcg cgcctcctgg gaagagagga      60
agcgggagag gagccacgt ctccgtgtcac ccaatatctc cagccgcgca gtcccgaaga      120
gtgtaagatg ttgcctgcgc ccaagctcgc ctgcaccccc tctctgatcc gagctggatc      180
cagagttgca tacagaccaa tttctgcatc agtggttatct cgaccagagg ctagtaggac      240
tggagagggc tctacggtat ttaatggggc ccagaatggt gtgtctcagc taatccaaag      300
ggagtttcag accagtgcaa tcagcagaga cattgatact gctgccaaat ttattggtgc      360
aggtgctgca acagtaggag tggctgggtc tgggtgctggt attggaacag tctttggcag      420
ccttatcatt ggttatgcc aaaaacccttc gctgaagcag cagctgttct catatgctat      480
cctgggattt gccttgtctg aagctatggg tctcttttgt ttgatggttg ctttcttgat      540
tttgtttgcc atgtaacaaa ttactgcttg acatgttggc attcatatta attacggatg      600
taattctgtg tatcttactg tgactccgaa aactgtagta ttggtgtcat gggaatgtac      660
gttatttcca aagtcatttc attaaagatg aaaactttaa aaaaaaaaaa aaaagggcgg      720
cc                                                                                   722
  
```

<210> 293  
 <211> 429  
 <212> DNA  
 <213> Homo Sapiens

```

<400> 293
atgttcgcct gcgccaagct cgcttcgacc ccctctctga tccgagctgg atccagagtt      60
gcatacagac caatttctgc atcagtgtta tctcgaccag aggctagtag gactggagag      120
ggctctacgg tatttaatgg ggcccagaat ggtgtgtctc agctaatacca aaggagattt      180
cagaccagtg caatcagcag agacattgat actgctgcca aatttattgg tgcagggtgct      240
gcaacagtag gagtggctgg ttctgggtgct ggtattggaa cagtctttgg cagccttctc      300
attggttatg ccagaaaccc ttcgctgaag cagcagctgt tctcatatgc tatcctggga      360
tttgcttgtg ctgaagctat gggctctctt tgtttgatgg ttgctttctt gattttgttt      420
gccatgtaa                                                                                   429
  
```

<210> 294  
 <211> 142  
 <212> PRT  
 <213> Homo Sapiens

```

<400> 294
Met Phe Ala Cys Ala Lys Leu Ala Cys Thr Pro Ser Leu Ile Arg Ala
 1             5             10             15
Gly Ser Arg Val Ala Tyr Arg Pro Ile Ser Ala Ser Val Leu Ser Arg
             20             25             30
Pro Glu Ala Ser Arg Thr Gly Glu Gly Ser Thr Val Phe Asn Gly Ala
             35             40             45
Gln Asn Gly Val Ser Gln Leu Ile Gln Arg Glu Phe Gln Thr Ser Ala
             50             55             60
Ile Ser Arg Asp Ile Asp Thr Ala Ala Lys Phe Ile Gly Ala Gly Ala
             65             70             75             80
Ala Thr Val Gly Val Ala Gly Ser Gly Ala Gly Ile Gly Thr Val Phe
             85             90             95
Gly Ser Leu Ile Ile Gly Tyr Ala Arg Asn Pro Ser Leu Lys Gln Gln
             100            105            110
Leu Phe Ser Tyr Ala Ile Leu Gly Phe Ala Leu Ser Glu Ala Met Gly
             115            120            125
Leu Phe Cys Leu Met Val Ala Phe Leu Ile Leu Phe Ala Met
             130            135            140
  
```

<210> 295  
 <211> 30  
 <212> DNA  
 <213> Homo Sapiens



<400> 295  
atggggccca gaatggtgtg tctcagctaa 30

<210> 296  
<211> 9  
<212> PRT  
<213> Homo Sapiens

<400> 296  
Met Gly Pro Arg Met Val Cys Leu Ser  
1 5

<210> 297  
<211> 18  
<212> DNA  
<213> Homo Sapiens

<400> 297  
atggtgtgtc tcagctaa 18

<210> 298  
<211> 5  
<212> PRT  
<213> Homo Sapiens

<400> 298  
Met Val Cys Leu Ser  
1 5

<210> 299  
<211> 21  
<212> DNA  
<213> Homo Sapiens

<400> 299  
atgccagaaa cccttcgctg a 21

<210> 300  
<211> 6  
<212> PRT  
<213> Homo Sapiens

<400> 300  
Met Pro Glu Thr Leu Arg  
1 5

<210> 301  
<211> 51  
<212> DNA  
<213> Homo Sapiens

<400> 301  
atgctatcct gggatttgcc ttgtctgaag ctatgggtct cttttgtttg a 51

<210> 302  
<211> 16  
<212> PRT  
<213> Homo Sapiens

<400> 302  
Met Leu Ser Trp Asp Leu Pro Cys Leu Lys Leu Trp Val Ser Phe Val  
1 5 10 15

<210> 303  
<211> 51

<212> DNA  
<213> Homo Sapiens

<400> 303  
atgggtctct tttgtttgat ggttgctttc ttgattttgt ttgccatgta a 51

<210> 304  
<211> 16  
<212> PRT  
<213> Homo Sapiens

<400> 304  
Met Gly Leu Phe Cys Leu Met Val Ala Phe Leu Ile Leu Phe Ala Met  
1 5 10 15

<210> 305  
<211> 33  
<212> DNA  
<213> Homo Sapiens

<400> 305  
atgggtgctt tcttgatttt gtttgccatg taa 33

<210> 306  
<211> 10  
<212> PRT  
<213> Homo Sapiens

<400> 306  
Met Val Ala Phe Leu Ile Leu Phe Ala Met  
1 5 10

<210> 307  
<211> 51  
<212> DNA  
<213> Homo Sapiens

<400> 307  
atgttggcat tcatattaat tacggatgta attctgtgta tcttactgtg a 51

<210> 308  
<211> 16  
<212> PRT  
<213> Homo Sapiens

<400> 308  
Met Leu Ala Phe Ile Leu Ile Thr Asp Val Ile Leu Cys Ile Leu Leu  
1 5 10 15

<210> 309  
<211> 74  
<212> DNA  
<213> Homo Sapiens

<400> 309  
atgggaatgt acgttatctc caaagtcatt tcattaaaga tgaaaacttt aaaaaaaaaa 60  
aaaaaaaaaggc ggcc 74

<210> 310  
<211> 24  
<212> PRT  
<213> Homo Sapiens

<400> 310  
Met Gly Met Tyr Val Ile Ser Lys Val Ile Ser Leu Lys Met Lys Thr

1 5 10 15  
Leu Lys Lys Lys Lys Lys Gly Arg  
20

<210> 311  
<211> 364  
<212> DNA  
<213> Homo Sapiens

<400> 311  
tcgacccacg cgtccggatt tagcaggaag ctgtgagagc agtttggttt ctagcatgaa 60  
gacagagccc caccctcaga tgcacatgag ctggcgggat tgaaggatgc tgtcttcgta 120  
ctgggaaagg gattttcagc cctcagaatc gctccacctt gcagctctcc ccttctctgt 180  
attcctagaa actgacacat gctgaacatc acagcttatt tcctcatttt tataatgtcc 240  
cttcacaaac ccagtgtttt aggagcatga gtgccgtgtg tgtgcgtcct gtcggagccc 300  
tgtctcctct ctctgtaata aactcatttc tagcagaaaa aaaaaaaaaa aaaaaagggc 360  
ggcc 364

<210> 312  
<211> 48  
<212> DNA  
<213> Homo Sapiens

<400> 312  
atgaagacag agccccaccc tcagatgcac atgagctggc gggattga 48

<210> 313  
<211> 15  
<212> PRT  
<213> Homo Sapiens

<400> 313  
Met Lys Thr Glu Pro His Pro Gln Met His Met Ser Trp Arg Asp  
1 5 10 15

<210> 314  
<211> 24  
<212> DNA  
<213> Homo Sapiens

<400> 314  
atgcacatga gctggcggga ttga 24

<210> 315  
<211> 7  
<212> PRT  
<213> Homo Sapiens

<400> 315  
Met His Met Ser Trp Arg Asp  
1 5

<210> 316  
<211> 18  
<212> DNA  
<213> Homo Sapiens

<400> 316  
atgagctggc gggattga 18

<210> 317  
<211> 5  
<212> PRT  
<213> Homo Sapiens

&lt;400&gt; 317

Met Ser Trp Arg Asp

1

5

&lt;210&gt; 318

&lt;211&gt; 99

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 318

atgctgtctt cgtactggga aagggatttt cagccctcag aatcgctcca ccttgagct

60

ctccccttct ctgtattcct agaaactgac acatgctga

99

&lt;210&gt; 319

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 319

Met Leu Ser Ser Tyr Trp Glu Arg Asp Phe Gln Pro Ser Glu Ser Leu

1

5

10

15

His Leu Ala Ala Leu Pro Phe Ser Val Phe Leu Glu Thr Asp Thr Cys

20

25

30

&lt;210&gt; 320

&lt;211&gt; 72

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 320

atgctgaaca tcacagctta tttcctcatt ttataaatgt cccttcacaa acccagtgtt

60

ttaggagcat ga

72

&lt;210&gt; 321

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 321

Met Leu Asn Ile Thr Ala Tyr Phe Leu Ile Phe Ile Met Ser Leu His

1

5

10

15

Lys Pro Ser Val Leu Gly Ala

20

&lt;210&gt; 322

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;400&gt; 322

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36

&lt;210&gt; 323

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;400&gt; 323

Met Ser Leu His Lys Pro Ser Val Leu Gly Ala

1

5

10

&lt;210&gt; 324

&lt;211&gt; 98

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

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 tttctagcag aaaaaaaaaa aaaaaaaaaa gggcggcc 98

<210> 325  
 <211> 32  
 <212> PRT  
 <213> Homo Sapiens

<400> 325  
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 1 5 10 15  
 Val Ile Asn Ser Phe Leu Ala Glu Lys Lys Lys Lys Lys Lys Gly Arg  
 20 25 30

<210> 326  
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 <212> DNA  
 <213> Homo Sapiens

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 ctaagctata ctaaccccag ggttggtcaa tttcgtgcc gccaccgcgg tcacacgatt 240  
 aacccaagtc aatagaagcc ggcgtaaaga gtgttttaga tcacccttc cccaataaag 300  
 ctaaaactca cctgagttgt aaaaaactcc agttgacaca aaatagacta cgaaagtggc 360  
 tttaacatat ctgaacacac aatagctaag acccaactg ggattagata cccactatg 420  
 cttagcccta aacctcaaca gttaaataca caaaactgct cgccagaaca ctacgagcca 480  
 cagcttaaaa ctcaaaggac ctggcgggtgc ttcatacccc tctagaggag cctgttctgt 540  
 aatcgataaa ccccgatcaa cctcaccacc tcttgctcag cctataatac gccatcttca 600  
 gcaaaccctg atgaaggcta caaagtaagc gcaagtaccc acgtaaagac gttagggtcaa 660  
 ggtgtagccc atgggggtggc aagaaatggg ctacattttc taccacagaa aactacgata 720  
 gcccttatga aacttaaggg tcgaagggtg atttagcagt aaactgagag tagagtgtct 780  
 agttgaacag ggccctgaag cgcgtagaca ccgcccgtca ccctcctcaa gtatacttca 840  
 aaggacattt aactaaaacc cctacgcatt tatatagagg agacaagtcg taacatggta 900  
 agtgactgg aaagtgcact tggacgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960  
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 aaaaaaaaaa aaaaaaaaaa gcggcc 1046

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<400> 327  
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 <212> DNA  
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 tag 63

<210> 330  
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<212> PRT  
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Val Ile Asn Leu  
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<210> 331  
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<212> DNA  
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<400> 331  
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ccacagctta aaactcaaag gacctggcgg tgcttcatac ccctctag 108

<210> 332  
<211> 35  
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<400> 332  
Met Leu Ser Pro Lys Pro Gln Gln Leu Asn Gln Gln Asn Cys Ser Pro  
1 5 10 15  
Glu His Tyr Glu Pro Gln Leu Lys Thr Gln Arg Thr Trp Arg Cys Phe  
20 25 30  
Ile Pro Leu  
35

<210> 333  
<211> 18  
<212> DNA  
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<400> 333  
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<210> 334  
<211> 5  
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<400> 334  
Met Lys Ala Thr Lys  
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<210> 336  
<211> 16  
<212> PRT  
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60/60

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1 5			
<210> 341			
<211> 152			
<212> DNA			
<213> Homo Sapiens			
<400> 341			
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa			120
aaaaaaaaaa aaaaaaaaaa aaaagggcgg cc			152
<210> 342			
<211> 50			
<212> PRT			
<213> Homo Sapiens			
<400> 342			
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1 5 10 15			
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys			
20 25 30			
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys			
35 40 45			
Gly Arg			
50			

**MICROORGANISMS**

Optional Sheet in connection with the microorganism referred to on pages 116-117, lines 18-31 and 1-12 of the description \*

**A. IDENTIFICATION OF DEPOSIT \***

Further deposits are identified on an additional sheet \*

Name of depositary institution \*

American Type Culture Collection

Address of depositary institution (including postal code and country) \*

10801 University Blvd.  
Manassas, VA 20110-2209  
US

Date of deposit \* March 16, 2000 Accession Number \* PTA-1492

**B. ADDITIONAL INDICATIONS \*** (leave blank if not applicable). This information is continued on a separate attached sheet**C. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE \*** (if the indications are not all designated States)**D. SEPARATE FURNISHING OF INDICATIONS \*** (leave blank if not applicable)

The indications listed below will be submitted to the International Bureau later \* (Specify the general nature of the indications e.g., "Accession Number of Deposit")

E. ☐ This sheet was received with the International application when filed (to be checked by the receiving Office)

\_\_\_\_\_  
(Authorized Officer)

☐ The date of receipt (from the applicant) by the International Bureau \*

was

\_\_\_\_\_  
(Authorized Officer)

Form PCT/RO/134 (January 1981)



# PATENT COOPERATION TREATY

## PCT

### DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rules 13ter and 39)

Applicant's or agent's file reference 10001-006-228	<b>IMPORTANT DECLARATION</b>	Date of mailing (day/month/year) <b>17 JUL 2001</b>
International application No.  PCT/US01/11655	International filing date (day/month/year)  09 APRIL 2001	(Earliest) Priority Date (day/month/year)  11 APRIL 2000
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.		
Applicant COGENT NEUROSCIENCE, INC.		

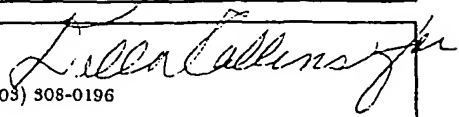
This International Searching Authority hereby declares, according to Article 17(2)(a), that **no international search report** will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
  - a. ☐ scientific theories.
  - b. ☐ mathematical theories.
  - c. ☐ plant varieties.
  - d. ☐ animal varieties.
  - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
  - f. ☐ schemes, rules or methods of doing business.
  - g. ☐ schemes, rules or methods of performing purely mental acts.
  - h. ☐ schemes, rules or methods of playing games.
  - i. ☐ methods for treatment of the human body by surgery or therapy.
  - j. ☐ methods for treatment of the animal body by surgery or therapy.
  - k. ☐ diagnostic methods practiced on the human or animal body.
  - l. ☐ mere presentations of information.
  - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☒ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
 

☒ the description
☒ the claims
☒ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out.
 

☒ the written form has not been furnished or does not comply with the standard.  
☐ the computer readable form has not been furnished or does not comply with the standard.
4. Further comments:  
Please See Continuation Sheet.

Name and mailing address of the ISA/US  
 Commissioner of Patents and Trademarks  
 Form PCT/ISA/203 (July 1998)\*  
 Washington, D.C. 20231

Authorized officer  
  
 MARY TUNG (703) 308-0196

DECLARATION OF NON-ESTABLISHMENT OF  
INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US01/11655

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

IPC(7): A61K 31/7088, 38/00, 39/395; C12N 1/20, 15/12; C12P 19/34, 21/06; G01N 33/53 US Cl.: 424/139.1; 435/7.1, 69.1, 91.1, 252.3, 320.1; 514/12, 44; 536/23.5

4. Further Comments (Continued):

A meaningful search cannot be performed on the instant claims.

The claims appear to encompass an unfathomable number of inventions because of the number of claimed sequences.

It is noted that the instant claim set is apparently drawn to a multitude of DNA or amino acid sequences shown in Figures 4-13. Each of Figures 4-13 are apparently broken up into a multitude of subfigures. Claim 1 (a) apparently refers to "an amino acid sequence which is shown in all of Figures 4A-AB". It is not at all clear how one sequence can be the same as all those separate, distinct sequences. Perhaps applicant intended to refer to the various subfigures in the alternative? Or maybe the open claim language "comprising" as in an amino acid sequence which comprises all of those shown in Figures 4A-AB.

Figures 4-13 are defective because the sheets are not numbered in consecutive Arabic numbers. See PCT/RO/106 mailed May 4, 2001. Further, the first sheet of each of the Figures 4-13 contains a heading "open reading frame for..." and the text "Fig No." These words are missing from the subsequent sheets of each of the subfigures 4-13. The figures are not clearly labeled. Further, with regard to the headings, PCT Rule 11.11(a) prohibits words in the drawings.

Each figure does not have a unique label which says "Fig. No. 4A, Figure No. 4B", etc. Some of the figures apparently contain subfigures which run over onto the next sheet. See 10L, 10J, etc. Further, some of the figures apparently contain subfigures which do not have a figure label, see the text in the box above Figure 10P. Furthermore, the numbering system of the sequences appears to be incorrect, see numbers 340 and 341, both denoting the same position of the last line of amino acids of Figure 10H. None of the aberrations are permissible and a search of any such material would not be meaningful.

Beyond all these errors, the overriding problem with performing a search on the claims is that in the figures and of the Brief Description of the Figures, pages 13-15, no SEQ ID Nos are provided. Without any such correlation, it is impossible to determine which of the sequences recited in the claims correspond to those recited in the sequence listing. Absent that correlation, it is impossible to determine the full scope of the claimed invention or to search even a portion of the claimed invention.

PCT Rule 6.2(a) states that the claims shall not, except when absolutely necessary, rely, in respect to the technical features of the invention, on references to the description of the drawings. In particular, they shall not rely on such references as "as described in part...of the description" or "as illustrated in figure...of the drawings". The nature of the instant invention does not meet the criteria of "absolutely necessary" because these claims could have easily been drafted to include the particular SEQ ID Nos of the sequences. That may result in the claim becoming rather lengthy, but this is to be expected when one claim appears to encompass hundreds of inventions.

The Authorized Officer contacted the applicants on 16 May 2001 concerning a potential Lack of Unity. However, upon further consideration, the claims have been determined to be unsearchable.